

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 14, 2003, 11:52:49 ; Search time 1953 Seconds
(without alignments)
16460.851 Million cell updates/sec

Title: US-09-884-2lla-2

Perfect score: 1985

Sequence: 1 ctaagaccgtggggaggcag.....gaaataaaaaaaaaaaaaa 1985

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estnu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_hic.*

9: gb_est1.*

10: gb_est2.*

11: gb_hic.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: gb_gss.*

18: em_gss_hum.*

19: em_gss_inv.*

20: em_gss_pln.*

21: em_gss_vrt.*

22: em_gss_fun.*

23: em_gss_mam.*

24: em_gss_mus.*

25: em_gss_other.*

26: em_gss_pro.*

27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
c 1	421.2	21.2	877	17	CNS02HJ0
c 2	397.2	20.0	905	17	CNS02K2T
c 3	297.4	15.0	1185	17	CNS02W1W
c 4	252	12.7	501	17	CNS03X7L
c 5	242.6	12.2	521	12	BF192805
c 6	234	11.8	1017	13	BI830442
					BI830442 603073302

7	222.6	11.2	1140	13	BM550365
8	217.8	11.0	833	12	BF973060
9	202.8	10.2	806	10	BE277142
10	175	8.8	981	9	AL552592
11	173.2	8.7	1081	13	BM549211
12	164.6	8.3	1108	12	BE744777
13	155.8	7.8	467	9	AI820754
14	154.6	7.8	788	12	BG114850
15	146.8	7.4	741	12	BG761088
16	144.8	7.3	570	12	BG085859
17	141.4	7.1	919	12	BG104273
18	139.6	7.0	570	10	BE389884
19	136	6.9	618	10	BE407321
20	135.6	6.8	937	14	BQ222929
c	129.6	6.5	637	17	AZ939737
22	128.6	6.5	1036	12	BG476740
23	113.8	5.7	935	13	BM424081
24	109	5.5	735	10	BB650258
25	108.4	5.5	1101	13	BM464123
26	107.2	5.4	676	10	BB624152
27	104	5.2	499	10	BE385328
28	104	5.2	957	14	BQ653378
29	103.2	5.2	711	10	BB631979
30	102.6	5.2	771	12	BG397084
31	96	4.8	441	10	BE629359
c	94.8	4.8	1000	13	BM476173
33	91	4.6	661	13	BM083450
c	85	4.3	352	12	BF416476
35	81	4.1	296	14	R72114
36	80.6	4.1	703	12	BF983238
c	77	3.9	989	17	CNS02UCU
38	76	3.8	952	12	BG437263
c	74.4	3.7	890	17	AZ530768
40	74.2	3.7	1025	14	BM911907
41	73.6	3.7	905	17	AZ550256
42	73.2	3.7	843	17	AZ551618
c	73.2	3.7	931	17	BH160272
44	73	3.7	662	13	BJ495713
c	73	3.7	795	17	AZ528485

ALIGNMENTS

RESULT 1	CNS02HJ0/c	CNS02HJ0	877 bp	DNA	linear	GSS 13-MAY-2000
LOCUS	Tetraodon nigroviridis genome survey sequence T7 end of clone					
DEFINITION	139P03 of library G from Tetraodon nigroviridis, genomic survey sequence.					
ACCESSION	AL197685					
VERSION	AL197685.1	GI:7835835				
KEYWORDS	GSS; genome survey sequence.					
SOURCE	Tetraodon nigroviridis.					
ORGANISM	Tetraodon nigroviridis					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.					
REFERENCE	1 (bases 1 to 877)					
AUTHORS	Roest-Crollius H., Jaillon O., Dasilva C., Bouneau L., Fisher C., Bernot A., Fizames C., Wincker P., Brottier P., Quetier F., Saurin W. and Weissenbach J.					
TITLE	Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence					
JOURNAL	Unpublished					
REFERENCE	2 (bases 1 to 877)					
AUTHORS	Roest-Crollius H., Jaillon O., Dasilva C., Fizames C., Fisher C., Bouneau L., Billault A., Quetier F., Saurin W., Bernot A. and Weissenbach J.					
TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis					
JOURNAL	Unpublished					

REFERENCE	3	(bases 1 to 877)	
AUTHORS		Genoscope.	
TITLE		Direct Submission	
JOURNAL		Submitted (12-APR-2000)	
COMMENT		This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon .	
FEATURES		Location/Qualifiers	
source		1. .877	
		/organism="Tetraodon nigroviridis"	
		/db_xref="taxon:99883"	
		/clone="139P03"	
		/clone_lib="g"	
		/notes="Genoscope sequence ID : COAG139CH021LP1-end : T7"	
BASE COUNT	203 a	193 c	299 g
ORIGIN		175 t	7 others
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		Best Local Similarity	73.9%; Pred. No. 3.2e-62;
		Matches	566; Conservative 6; Mismatches 189; Indels 5; Gaps 3;
QY	644	CGTGGCAATGACCAAGAAGAACTGTCACATCACCATGTACTTTTTCATCTGTAGCCT	703
Db	877	CGCTGTATAGTCAAGACAAAGACCTCCACTGCCCATGTATTTTTCATCTGCAGCCT	818
QY	704	GGCTGTGGCGATATGCTGTGTAGCGTTTCCAAACGGGTC-AGAGACCATGTCATCACCC	762
Db	817	GGCGGTGGCGACATGTGTGTAGCKTCTCCAAACGGCTCGGGAGACTATCGTCTACGCGC	758
QY	763	TGTTGAAC---AGTAGGATACGGACGGCGCAGAGTTTCAGGTGATATGATATGTC	819
Db	757	TCATCAAGGGGCGACGCTGACATCCCGCAAGGCTGATCAAAAGCATGSAACAGCTCT	698
QY	820	TTGACATCGGTATCTAGTCTCTGCTCGCTCGATTTGCAGCTGCTCTCAATTCGAG	879
Db	697	TTGACTCCATGATCTCAGCTCTCTGTGGCGTCAATCTGCACCTCTGCGCATCGCG	638
QY	880	TGACAGGTACTTTTACTATCTTTTATGCCCCATACCATAACATCATGACGGTGAGGC	939
Db	637	TCGATCGTTACATCACCATCTTCTAGCGCTGCGCTACCAACATCGTCACCCCTCGCA	578
QY	940	GGTTTGGGATCATCATCAGTTGCATCTGGCGGCTTGCAGGTGTGAGCATCTTTCTTCA	999
Db	577	GAGCCTCGCTGGTTCATCAGCAGCATCTGACCTGTGCAACCTGTGCGCGCTCTTCA	518
QY	1000	TCATTTACTCGGACAGTACTGTGTCTATCATCTGCTCATCACCA-TCGTTCTTCCACATG	1058
Db	517	TCATCTACTCGGAGACACACCGTCTCATCTGCTCATCACCACTTTCTTCCACATG	458
QY	1059	CTGGCCCTCATGGCTTCTCTTACGTCACATGTTCTCTCATGCCCCAGACTGCACATCAAG	1118
Db	457	CTGGTGCTCATGGCTCTCTGAACGTGCACATGTTTCTGCTGGCGGCTGCACATGAAG	398
QY	1119	AGAAATCGCGCTCTCCCGGACCGCCACCATCCCGCAAGGGGCCAATGAAGGGTGCC	1178
Db	397	CGGATCGCGCGCATGCGGGCAACCGCCCATCCACAGAGGGGCCAATGAAGGGCGCC	338
QY	1179	ATTACCTTGACCATACTCATTTGGGTCTTCGTCTGCTGCTGGCTTCTTCTCTCCAC	1238
Db	337	ATCACCTTCACCATCTCTCTGGAGTGTGTGGTGTGCTGGGCACTTCTTCTCTCCAC	278
QY	1239	TTGATATTTACATCTCTTGTCCCGAATCATCTATGTTGTGTTCTATGTCCTACATTT	1298
Db	277	CTCATCTCTCATGATCACCTGCCCCAAGAACCCTACTGCACCTGCTTCTATGTCGACATC	218
QY	1299	AACTTGTACCTCATCTGTATGATGTGTAACTCCATTCGACCCCTCATTTATGCATCTC	1358
Db	217	AACATGTACCTCATCTCATATGTCACATCCGTCATCGACCCCATCATCTTACGCCCTTC	158
QY	1359	CGGAGCCCAAGCTGAGGAAACCTTCAAGAGATCATCTGTGTCT	1404
Db	157	CGCAGCCAGGAGATGAGGAAGACCTTCAAGGAGATCTTCTGCTGCT	112

CNS02KZT

905 bp

DNA

linear

GSS 14-MAY-2000

Tetraodon nigroviridis genome survey sequence T7 end of clone 146B21 of library G from Tetraodon nigroviridis, genomic survey sequence.

AL202178

1

GI:7860523

GSS: genome survey sequence.

Tetraodon nigroviridis

Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

1 (bases 1 to 905)

Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.

Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

Unpublished

2 (bases 1 to 905)

Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.

Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

Unpublished

3 (bases 1 to 905)

Genoscope.

Direct Submission

Submitted (12-APR-2000)

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

Location/Qualifiers

1. .905

/organism="Tetraodon nigroviridis"

/db_xref="taxon:99883"

/clone="146B21"

/clone_lib="g"

/notes="Genoscope sequence ID : COAG146CALLP1-end : T7"

BASE COUNT

225 a

202 c

305 g

172 t

1 others

Query Match

20.0%; Score 397.2; DB 17; Length 905;

Best Local Similarity

73.9%; Pred. No. 3.9e-58;

Matches

517; Conservative 1; Mismatches 179; Indels 3; Gaps 1;

QY

708

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767

Db

905

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846

QY

768

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824

Db

845

AACGGGGGACCGCTGACCATCCCGCAAGGCTGATCAAAAGCATGACAACTGCTTTGAC

786

QY

825

TCGGTGTCTGTAGTCTCTTGTCTGCTCGCTCGATTTTGACGCTCTCTCAATTGCAGTGGAC

884

Db

785

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726

QY

885

AGGTACTTACTATCTTTTATGCCCTCCAGTACCATAACATCATGACGGGTGAGCGGGTT

944

Db

725

CGTTACATCACCATCTTCTACGCCCTGGCTACCAACATCGTCAACCTGCGCAGAGCC

666

QY

945

GGGATCATCATGATGTCATCTGGCGGCTTGCAGGTGTGACGATCTTGTTCATCTT

1004

Db

665

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606


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Db 315 TGGCGGAGGATGAACCAACCCATCACCATGGAATGCATATCTCTCCACTTCTGGAAC 374
Qy 498 CGCAGCACCTACGACAGCAGCGCAAGCCACTAGTCCCTTGGCAAGGCTACCCGAC 557
Db 375 CGCAGCACCTACGACAGCAGCGCAAGTGCAGCCCTTGGAAAGGCTACTTGAA 434
Qy 558 GGGGAGTCTACGACGAACTCTTCTGCTCCCGGAGGTGTTCTGACTCTGGGGTCTATA 617
Db 435 GGAGGATGCTACGAGCAACTTTTGTCTCTCTCTGAGGTGTTGTGACTCTGGGTGCTATA 494
Qy 618 AGCTTGTCTGAGAACATCTCGGTGAT 643
Db 495 AGCCTGTTGGAGAACATCTCGGTGAT 520

RESULT 6
BI830442/c
DEFINITION 603073302f1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5165137 5',
mRNA sequence.
ACCESSION BI830442
VERSION BI830442.1 GI:15941992
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1017)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1410 row: d column: 02
High quality sequence stop: 794.
FEATURES
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/clone="IMAGE:5165137"
/clone_lib="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dr primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."
BASE COUNT 278 a 224 c 297 g 218 t
ORIGIN
Query Match 11.8%; Score 234; DB 13; Length 1017;
Best Local Similarity 61.2%; Pred. No. 2.3e-30;
Matches 459; Conservative 0; Mismatches 265; Indels 26; Gaps 4;
Qy 646 TGGCAATAGGCAAGCAAGAAATCTG-CACCTACCCCATGTACT-TTTCATCTCTAGCCT 703
Db 729 TGCTGTGTTCAAGAAATAGTATCTGCCAGCACCCCATGTACTTTTTTCATCTGATCT 670
Qy 704 GGCTGTGGCCGATATGCTGGTGGAGCTTTCCACAGCGGTTCAGAGACCATCGTCAACCCCT 763
Db 669 GGCCATATCTGATATGCTGGGACGCTTATAGATCTTGAAATATCTTGATCATATT 610
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Qy 764 GTTGAACAGTACGATACGGAGCGCGAG---AGTTTCACGGTGAATATTGATATTTGATGTCAT 820
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Qy 821 TGACTCGGTGATCTGTAGCTCCTTGTCTCGCTCGATTTTGCAGCCCTGCTCTCAATTGTCAGT 880
Db 549 CGACTCCCTGTTTGTCTCTCCCTGCTTGGTCCATCTTTCAGCCCTGCTGTGATTTGCTGTC 490
Qy 881 GGACAGGTACTTACTATATCTTTTATGCCCTCCAGTACCATACATCATCAGCGGTGAGCGG 940
Db 489 GGACCGCTACATCACCATCTTCCACGCACTCGGTACCAACGATCGTGACCATCGCGCG 430
Qy 941 GGTGGGATCATCATCATCAGTTTCATCTGGCGCTTGCACGGTGTGCAGCGTCTTCTTTCAT 1000
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Db 309 GGTCTTTCATCTGCTCTCTATGTGCACATGTTCTGCTGTGCTGCATGCCACACGAGAA 250
Qy 1121 AATCGCGTCTCTCCGGCACCGGCACCATCGCCAAAGGGCCAAACATGAAGGGTGCCAT 1180
Db 249 GATCTCCACCTCTCCCGA-----GCCAACATGAAGGGGCCAT 211
Qy 1181 TACCTTGACCATACTCAATTGGGGTCTTCTGCTGTCTGCTGGGCTCCATCTTCTCCACATT 1240
Db 210 CACACTGACCATCTGCTCGGGGTCTTCATCTTCTGCTGGGCCCCCTTGTGCTTTCATGT 151
Qy 1241 GATATTTACATCTCTTGTGCCAGAAATCCATATCATGTGTGTGCTTCATGTCTCACTTAA 1300
Db 150 CCTCTTGATGACATTTCTGCCCAAGTAACCCCTACTGCGCTGCTACATGTCTCTTCCA 91
Qy 1301 CTTGTACTCTATTCTGATCATGTGTAACTCCATCATCGACCTCTCAATTATGACACTCG 1360
Db 90 GGTGAAGGCGATGTTGATCATGTGCAATCCCGTATTCACCCCTTCATATATGCTTCGG 31
Qy 1361 GAGCAAGAGCTGAGGAAAACCTTCAAGA 1390
Db 30 GAGCCAGAGCTCAGGAGCGCATTCAAAAA 1
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LOCUS BI850365
DEFINITION AGENCOURT_6542025 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5549166
5', mRNA sequence.
ACCESSION BI850365
VERSION BI850365.1 GI:18786509
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1140)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12259 row: e column: 07
High quality sequence stop: 622.
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FEATURES source

Location/Qualifiers

1. .1140

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5549166"

/clone_lib="NIH_MGC_72"

/tissue_type="melanotic melanoma"

/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."

210 a 395 c 290 g 244 t 1 others

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 11.2%; Score 222.6; DB 13; Length 1140;

Matches 397; Conservative 0; Mismatches 269; Indels 3; Gaps 1;

QY 746 GACCATCGTCATCACCCCTGTGAACAGTACGGATACGGACGCGCAGAGTTTCACGGTGAA 805

Db 22 GGCGGTCACTCCTCTGTGAGCGCGTGCACGTGTGGCGCGGCTGCGTGCTGCAGCA 81

QY 806 TATTGATATGTCATTCGCTGATCTGTAGCTCCTTGTCTCGCTCGATTTGCAGCCT 865

Db 82 GCTGGACAATGTCATTCGCTGATCACCTGCAGCTCCATGCTGCAGGCTCTGCTTCT 141

QY 866 GCTCTCAATTCAGTCGACAGGTACATTTACTATCTTTTATGCTCCTCCAGTACCATAACAT 925

Db 142 GGGCGCCATCGCGGTGACCGGTACATCTCCATCTTCTAGGCACTCGGTACACAGCAT 201

QY 926 CATGACGGTGAGCGGGTGGGATCATATCATATGTCATCTGGGGGGTTCGACGGTGTG 985

Db 202 CCGTACCCCTGCGCGCGCGCGGAGCCGTGTGGGCGCATCTGGGTGGCAGTGTCTCTT 261

QY 986 AGGCATCTTGTTCATCATATTTACTCGACAGTACTGCTGTCATCATCTGCTCATCAAT 1045

Db 262 CAGCAGCTCTTCATCGCTACTACGACACGCTGGCGGCTGCTGCTGCTGCTGCTT 321

QY 1046 GTTCTTCACCATGCTGGCCCTCATGGCTTCTCTACGTCCACATGTTCTCTCATGGCCAG 1105

Db 322 CTTCTGGCTATGCTGTGCTCATGCGCGTGTGTAGTCCACATGCTGGCGCGGCTG 381

QY 1106 ACTGCACATCAGAGATCGCC---GTCTCCGGGCGACCGACCATCGGCCAAGGGCG 1162

Db 382 CCAGCAGCGCCAGGGCATCGCGGCTCCACAGAGCAGCGCGCGGTCCACGAGGGCTT 441

QY 1163 CAACATGAAGGTGCCATTAACCTTGACCATACTCATTTGGGTCCTGCTGCTGCTGGCG 1222

Db 442 TGGCCTTAAGGCGTGTACCCCTACCAATCTGCTGGGCATTTTCTTCTCTGCTGGGG 501

QY 1223 TCATTTCTTCTCCATTTGATATTTACATCTCTTTGCCAGAAATCCATCTGTGTGTG 1282

Db 502 CCGCTTCTTCTGTCATCTCACACTCATCTGCTCTGCGCCGAGACCCACGTCGGGTG 561

QY 1283 CTTCAATGCTCACTTTAACTTGTACTCTATTCATGTCATGTCATCTCAATCATCGACCC 1342

Db 562 CATCTTCAAGAACTTCAACCTTTCTGCCCTCATCATCTGCAATGTCATCATCGACCC 621

QY 1343 TCTCATTTATGACCTCCGAGCGCAAGAGCTGAGGAAACCTTCAAGAGATCATCTGTG 1402

Db 622 CTTCTATTCAGCTTCCACAGCAGAGCTCCGAGGAGCTCCAGGAGGTGCTGACATG 681

QY 1403 CTATCCTCT 1411

Db 682 CTCCTCTGCT 690

RESULT 8

BF973060

LOCUS

DEFINITION

BF973060

602241386F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4330124 5',

mRNA sequence.

BF973060

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Accession

BF973060.1

GI:12340275

EST.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 833)

NIH-MGC <http://imgc.ncl.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cyapbs-re@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://imgc.llnl.gov>

Plate: LLCM1192 row: k column: 21

High quality sequence stop: 780.

Location/Qualifiers

1. .833

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4330124"

/clone_lib="NIH_MGC_46"

/tissue_type="leiomyosarcoma cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

117 a 295 c 230 g 191 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 11.0%; Score 217.8; DB 12; Length 833;

Matches 449; Conservative 0; Mismatches 282; Indels 12; Gaps 5;

QY 577 TCTTGCTCTCCCGGAGGTGTTCGTGACCTCTGGGGTCATAAGCTTGTCTGGAGAACATTC 636

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QY 637 TGGTGATCTGTGCAATAGCCAAAGAAATCTGCACCTCACCCATGTACTTTTTCATCT 696

Db 65 TGGTGTGGCCACCATCGCCAGAACCGGAACCTGCACCTACCCATGTACTGCTTCATCT 124

QY 697 GTAGCCTGCTGTGGCCGATATGCTGGTGAGCGTTTCCAAACGGGTTCAGACCATCGTCA 756

Db 125 GCTGCTGCGCTTGTGCGACCTGCTGCTGAGCGGGAACGCTGCTGGAGAGCGCGCTCA 184

QY 757 TCACCTCTGTGAA---CAGTACGGATACGAGCGCCAGAGTTTCACGGTGAATATTGATA 813

Db 185 TCCTCTGCTGGTGGCGCGGTGCACGTGGGCGCGGCTGCGGTGCTGCGAGCTGGGACA 244

QY 814 ATGTCAATGACCTGCGTGATCTGTAGCTCCTTCTGCTCGCTTCGATTTTGCACCCCTGCTCTCAA 873

Db 245 ATGTCAATGACCTGCGTGATCTGTAGCTCCTTCTGCTCGCTTCGATTTTGCACCCCTGCTCTCAA 304

QY 874 TTGCAGTGGACAGGTACTTTTACTATCTTTTATGCGCTTCCAGTACCATAACATCATGACGG 933

Db 305 TCGCGTGGACCGCTTACATCTCTCATCTTCTAGCAGCTGCGCTTACCACAGCATCGTGACCC 364

QY 934 TGAGCGGGTGGGATCATCATCTGTCATCTGCGCGGCTTGCACGGGTGTCAGGCATCT 993

Db 365 TGCCCGGGCGCGGCGGCGGCTTGGGGCCATCTGGGTGGCCAGTGTGCTCTTCACAGCCG 424

Matches	364;	Conservative	0;	Mismatches	227;	Indels	5;	Gaps	2;
QY	546	GGCTACCCCGAGGGGATGCTACGAGCAACTCTTCGTCTCTCCCGGAGGTGTTCGTGACT	605						
Db	157	GCAACACGACAGAGCCGGTGCCTTGAGGGTGCATCTCTGACGGGCTCTTCCTCAGC	216						
QY	606	CTGGGGGTCTAAGCTTGTGAGAAACATCTTCGTGGTATCTGTGGCAATACGCAAGACAAG	665						
Db	217	CTGGGGCTGTGAGCTTGTGTGAGAACGCGCTGGTGGCGCCACCATCCGCCAAGAACCGG	276						
QY	666	AATCTGCACTCAACCATGTACTTTTTCATCTCFAGCTGGCTGTGGCCCATATGCTGGTG	725						
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Db	337	AGCGGAGCAAGTGTCTGGAGAGCGCGTTCATCTCTGCTGGAGCCCGTGCATCTGGTG	396						
QY	783	GACGGCAGAGTTTTCACGGTGAATATTTGATAATGCAATTTGACTTGGGTGATCTGAGTCC	842						
Db	397	GCCCGGGCTGCGGTCTGCAGCAGCTGGACAAATGTATTGAGTGTATCATCTACCTGCAGCTCC	456						
QY	843	TTGCTCGCTCGATTTGACGCTGCTCTCAATTTGAGTGGACAGGTACTTTATATATCTTT	902						
Db	457	ATGCTGTCCAGCTCTGCTTCTCTGGCGCCATCGCGCTGACATCTCCATCTTCATCTTC	516						
QY	903	TATGCCCTCCAGTACCATAAATCATGACGGTGGAGCGGTGGGATCATCATCATGTTGC	962						
Db	517	TACGCACTCGCTACCAACAGCATGTCACCTTCCGCGGCGGCGGAGCCGCTTGGCGGC	576						
QY	963	ATCTGGGGCGGTTCACGGTGTGACGATCTTTGTTCAATCATTTTATTCGACAGTACTGCT	1022						
Db	577	ATCTGGGTGGCAGTGTCTCTTTCAGCAGCTCTTTCATCGCCTACTTACGACCAACGCTGCC	636						
QY	1023	GTCATCATCTGCTCATCACCATGTTCTTCACCATGCTGGCCCTCATGCTTCTCTCTAC	1082						
Db	637	GTCTGCTGCTGCTCTGCTGCTGCTTCTTCCTGGTATGCTGCTCATGCGCGCTGTGATC	696						
QY	1083	GTCCACATGTTCTCATGGCCAGACTGCACATCAAGAGAAATCGCGCTCTCCCGGG	1138						
Db	697	GTCCACATGCTGGCC--GGGCTGACGACGCCAGGCATCGCGGTCCACAGAG	750						
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AL552592									
LOCUS	AL552592	LTI_NFL006_PL2	981 bp	mrna	linear	EST	16-FEB-2001		
DEFINITION									
ACCESSION									
VERSION									
KEYWORDS									
SOURCE									
ORGANISM									
REFERENCE									
AUTHORS									
JOURNAL									
COMMENT									
FEATURES									
source									
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/clone_lib="NIH_MGC_20"									
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/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."									
BASE COUNT	121 a	270 c	248 g	167 t					
ORIGIN									
Query Match									
Best Local similarity	10.2%;	Score 202.8;	DB 10;	Length 806;					
Query	61.1%;	Pred. No. 5e-25;							

cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com

BASE COUNT 171 a 299 c 327 g 179 t 5 others
ORIGIN

Query Match 8.8%; Score 175; DB 9; Length 981;
Best Local Similarity 60.3%; Pred. No. 2.6e-20;
Matches 319; Conservative 3; Mismatches 203; Indels 4; Gaps 2;

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QY 546 GGTACCCGACGGGGATGCTACGAGCAACTCTTCTCTCCCGGAGGTGTTCTCGTACT 605
Db 454 GCGAACCAGACGAGCGCCGGTGCCTGGAGGTCTCCATCTCTACGGGCTCTTCCCTCAGC 513
QY 606 CTGGGGTCTAAGCTTGTGGAGAACATCTCGGTATGCTGGCAATAGCCAAAGACAAG 665
Db 514 CTGGGGTGTGAGCTTGTGGAGAACGCGCTGGTGGCCACCACATCGCCAAAGACCGG 573
QY 666 AATCTGCATCACCCATGACTTTTTCATCTGTAGCTGTGGCTGTGCCGATATGCTGGTG 725
Db 574 AACTCGCATCACCCATGACTTCTTCATCTGTCTGTGGCTGTGGCTGTGGACCTGCTGGTG 633
QY 726 AGCGTTTCCAAACGGGTGAGAGACCATCGTCATCACCCCTGTGTAA---CAGTAGCGATACG 782
Db 634 AGCGGAGCAACGTCGTGGAGAGCGCGCTCATCTCTCTGTGGAGCGCGTGCACCTGGTG 693
QY 783 GACGCGCAGATTTCACGCTGATATGATATGATATGATGTCATGTCGCTGATCTGTACTCTC 842
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QY 843 TTGCTCGCTCGATTGTCAGCTGCTCTCAATTGCAGTGGACAGGTACTTTTACTATCTTT 902
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QY 903 TATGCCCTCCAGTACCATAACATCATGACGGTGGAGCGGTGGGATCATCATCATCATGTC 962
Db 814 TAGGCACTCGGTACCACAGCATCGTGACCCCTGCGCGGCGCGGCGGTGCGGCC 873
QY 963 ATCTGGCGGCTTGACAGGTGTGACGATCTTGTTCATCATTTACTTCGACAGTACTGCT 1022
Db 874 ATCTGGGTGSGCATGTCTCTCTTCARCACGCTCTTCTATCGCTTACTTAMGACACCGTGGCC 933
QY 1023 GTCATCATCTGCTCATACCATGTTCTTTCACCATGCTGCGCCCTCATGG 1071
Db 934 GTCTCTGCTGCTGCTGCTGCTC-TCTTCTGGTATGCTGTGCTCATGG 981
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RESULT 11
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LOCUS AGENCOURT_5558414 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5548486
DEFINITION 5', mRNA sequence.
ACCESSION BM549212
VERSION BM549212.1 GI:18784430
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1081)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: L1AM12257 row: h column: 23
High quality sequence stop: 707.
Location/Qualifiers
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/note="Organ: skin; Vector: pCMV-Sport6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2 kb. Library constructed by Life Technologies."

BASE COUNT 171 a 347 c 348 g 211 t 4 others
ORIGIN

Query Match 8.7%; Score 173.2; DB 13; Length 1081;
Best Local Similarity 60.6%; Pred. No. 5.1e-20;
Matches 335; Conservative 0; Mismatches 211; Indels 7; Gaps 3;

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QY 546 GGCTACCCGACGGGGATGCTACGAGCAACTCTTCTCTCCCGGAGGTGTTCTCGTACT 605
Db 364 GCGAACCAGACGAGCGCCGGTGCCTGGAGGTCTCCATCTCTACGGGCTCTTCCCTCAGC 423
QY 606 CTGGGGTCTAAGCTTGTGGAGAACATCTTCTGTGATCTGTCGCAATAGCCAAAGACAAG 665
Db 424 CTGGGGCTGAGGAGCTTGTGGAGAACGCGCTGGTGGCCACCACATCGCCAAAGACCGG 483
QY 666 AATCTGCATCACCCATGACTTTTTCATCTGTAGCTGTGGCTGTGGCGGATATGCTGGTG 725
Db 484 AACTCGCATCACCCATGACTTCTTCATCTGTCTGTGGCTGTGGACCTGCTGGTG 543
QY 726 AGCGTTTCCAAACGGGTGAGAGACCATCGTCATCACCCCTGTGTAA---CAGTAGCGATACG 782
Db 544 AGCGGAGCAACGTCGTGGAGAGCGCGCTCATCTCTCTGTGGAGCGCGTGCACCTGGTG 603
QY 783 GACGCGCAGATTTCACGCTGATATGATATGATATGATGTCATGTCGCTGATCTGTACTCTC 842
Db 604 GCGCGGGCTGCGGTGCTGCAGCAGCTGGACAAATGTCACTGACGTGATCACTCAGCTCC 663
QY 843 TTGCTCGCTCGATTGTCAGCTGCTCTCAATTGCAGTGGACAGGTACTTTTACTATCTTT 902
Db 664 ATGCTGTCCAGCTCTGCTTCTTCCGCGGCATCGCCGTGGACCATACATCTCCATCTTC 723
QY 903 TATGCCCTCCAGTACCATAACATCATGACGGTGGAGCGGTGGGATCATCATCATCATGTC 962
Db 724 TAGGCACTCGGTACCACAGCATCGTGACCCCTGCGCGGCGCGGCGGTGCGGCC 783
QY 963 ATCTGGCGGCTTGACAGGTGTGACGATCTTGTTCATCATTTACTTCGACAGTACTGCT 1022
Db 784 ATCTGGGTGSGCATGTCTCTTTCACCATGCTGCGCCCTCATGGTCTCT-CT 1078
QY 1023 GTCATCATCTG---CCTCATCACCATGTTCTTTCACCATGCTGCGCCCTCATGGTCTCT-CT 1078
Db 844 CGTCTGNNCTGTGGCCCTCGTGGTCTTCTTCTTCTGGGTATGCTGGNGCTCATGGCCCGTCT 903
QY 1079 CTACGTCCACATG 1091
Db 904 GTACGTCCACATG 916
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RESULT 12
BE744777
LOCUS BE744777
DEFINITION mRNA sequence.
ACCESSION BE744777
VERSION BE744777.1 GI:10158756
KEYWORDS EST.

BE744777 1108 bp mRNA linear EST 15-SEP-2000
601573166F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834185 5',
mRNA sequence.
BE744777
BE744777.1 GI:10158756
EST.


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EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGCAG(G). Size-selected >500bp for average insert size  
1.8kb. Library constructed by Ling Hong in the laboratory  
of Gerald M. Rubin (University of California, Berkeley)  
using ZAP-cDNA synthesis kit (Stratagene) and Superscript  
II RT (Life Technologies). Note: this is a NIH_MGC  
Library. |"
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BASE COUNT 123 a 239 c 215 g 164 t
ORIGIN

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Query Match 7.48; Score 146.8; DB 12; Length 741;  
Best Local Similarity 60.18; Pred. No. 1.8e-15;  
Matches 262; Conservative 0; Mismatches 172; Indels 2; Gaps 1;  
  
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QY 1031 CTGCCTCATCACCATGTTCTTACCATGCTGGCCCTCATGGCTTCTCTACGTCCACAT 1090  
Db 1 CTGCCTCATCACCATGTTCTTACCATGCTGGCCCTCATGGCTTCTCTACGTCCACAT 1090  
  
QY 61 GTGCTGTGTGCTTCTTCTGCTATGCTGTGCTCATGTGCTGCTGTGCTGCTGCTGCTGCT 120  
Db 1 GTGCTGTGTGCTTCTTCTGCTATGCTGTGCTCATGTGCTGCTGCTGCTGCTGCTGCTGCT 120  
  
QY 1091 GTTCTCATGGCAGACTGCACATCAAGAGAAATGCGCG--TCCTCCCGGCGACCGGCAAC 1148  
Db 1 GTTCTCATGGCAGACTGCACATCAAGAGAAATGCGCG--TCCTCCCGGCGACCGGCAAC 1148  
  
QY 121 GCTGGCCCGGCGCTGCCAGCACGCCAGGATGCCCGGCTCCACAAAGAGCGCGCG 180  
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QY 241 TTCTCTGTGCTGGGCGCCCTTCTTCTGCTATCTCACACTCATGCTCTGCGCGAGCAC 300  
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Db 1 CCATACGTGTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1328  
  
QY 301 CCCACGTGCGGCTGCATCTTCAAGAACTTCAACCTTTCTCGCCCTCATCATCTGCAAT 360  
Db 1 CCCACGTGCGGCTGCATCTTCAAGAACTTCAACCTTTCTCGCCCTCATCATCTGCAAT 360  
  
QY 1329 TCCATCATGACCCCTCTCATTTATGCACTCGGAGCCAGAGCTGAGGAAACCTTCAA 1388  
Db 1 TCCATCATGACCCCTCTCATTTATGCACTCGGAGCCAGAGCTGAGGAAACCTTCAA 1388  
  
QY 361 GCCATCATGACCCCTCTCATTTATGCACTCGGAGCCAGAGCTGAGGAAACCTTCAA 420  
Db 1 GCCATCATGACCCCTCTCATTTATGCACTCGGAGCCAGAGCTGAGGAAACCTTCAA 420  
  
QY 1389 GAGATCATCTGTGCT 1404  
Db 1 GAGATCATCTGTGCT 1404  
  
QY 421 GAGGTGCTGACGTGCT 436  
Db 1 GAGGTGCTGACGTGCT 436
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Search completed: June 14, 2003, 13:24:15
Job time : 1967 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 4, 2003, 18:03:31 ; Search time 51 Seconds
(without alignments)
867.435 Million cell updates/sec

Title: US-09-884-211a-3

Perfect score: 1728

Sequence: 1 MNSTHHGHMHTSLHFNWST.....FKRIICCYPLGGICDLSSRY 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1728	100.0	332	23	Feline melanocortin
2	1685	97.5	332	23	Canine melanocortin
3	1659.5	96.0	332	18	Melanocortin-4 rec
4	1659.5	96.0	332	19	Melanocortin-4 rec
5	1659.5	96.0	332	19	Human melanocortin
6	1659.5	96.0	332	20	Human MC4 protein.
7	1659.5	96.0	332	21	A human melanocort
8	1659.5	96.0	332	21	Synthetic labeled
9	1659.5	96.0	332	22	Amino acid sequenc
10	1653.5	95.7	332	21	Human G protein co

11	1653.5	95.7	332	23	AAE15746	Human melanocortin
12	1648.5	95.4	332	21	AAE02857	Human G protein co
13	1645.5	95.2	332	21	AAE94301	Rhesus monkey mela
14	1632.5	94.5	332	21	AAE83182	Melanocortin recep
15	1617.5	93.6	332	21	AAE87415	Melanocortin-4 rec
16	1613.5	93.4	332	19	AAW37831	Human melanocortin
17	1613.5	93.4	332	20	AAW42377	Human melanocortin
18	1613.5	93.4	332	19	AAW87869	Homo sapiens mutan
19	1611.5	93.3	332	19	AAW42378	Homo sapiens mutan
20	1604.5	92.9	332	19	AAW42379	Homo sapiens mutan
21	1465	84.8	311	22	AAU08750	Human melanocortin
22	1407	81.4	293	21	AAE83184	Melanocortin recep
23	1266	73.3	248	21	AAE78931	Porcine melanocort
24	1261	73.0	248	22	AAU08751	Porcine melanocort
25	1250	72.3	248	21	AAU78932	Porcine melanocort
26	1047	60.6	325	16	AAE79501	Rat melanocortin r
27	1030	59.6	325	19	AAE37833	Mouse melanocortin
28	1030	59.6	325	20	AAW87870	Mouse melanocortin
29	1027	59.4	325	18	AAW19705	Melanocortin-5 rec
30	1027	59.4	325	19	AAE79688	Melanocortin-5 rec
31	1027	59.4	325	19	AAW41067	Mouse melanocortin
32	1027	59.4	325	19	AAW33725	Mouse melanocortin
33	1027	59.4	325	20	AAE92443	Mouse MC5 protein.
34	1027	59.4	325	21	AAE18770	A human melanocort
35	1024.5	59.3	325	21	AAE94266	Rhesus monkey mela
36	1023.5	59.2	325	16	AAE79502	Human melanocortin
37	1000.5	57.9	323	21	AAE94427	Rhesus monkey mela
38	1000.5	57.9	323	22	AAE60968	Murine melanocorti
39	1000.5	57.9	323	23	AAE20595	Mus musculus melan
40	997.5	57.7	325	15	AAE49726	Sequence of a poly
41	988.5	57.2	360	23	AAU95520	Human olfactory an
42	987.5	57.1	360	18	AAW19703	Melanocortin-3 rec
43	987.5	57.1	360	19	AAE79686	Melanocortin-3 rec
44	987.5	57.1	360	19	AAE33723	Human melanocortin
45	987.5	57.1	360	20	AAE92441	Human MC3 protein.

ALIGNMENTS

RESULT 1	
AAU76427	
ID	AAU76427 standard; Protein; 332 AA.
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AC	AAU76427;
XX	
DT	08-MAY-2002 (first entry)
XX	
DE	Feline melanocortin 4 receptor (MC4R).
XX	
KW	Melanocortin 4 receptor; MC4R; G-protein coupled; receptor; cat;
KW	appetite; metabolic disorder; cachexia; anorexia;
KW	weaning-induced inappetence; growth; diabetes; cancer; renal failure;
KW	cardiac disease; endotoxaemia; fever; hepatic lipodosis; infection;
KW	inflammation; post partum sow; dairy cow; livestock; poultry;
KW	shipping stress; crowding stress; obesity; vaccine.
XX	
OS	Felidae.
XX	
PN	EP1167386-A1.
XX	
PD	02-JAN-2002.
XX	
PF	26-JUN-2001; 2001EP-0305509.
XX	
PR	26-JUN-2000; 2000US-213909P.
XX	
PA	(PFIZ) PFIZER PROD INC.
XX	
PI	Hickman MA, Houseknecht KL, Robertson AS;
XX	
DR	WPI; 2002-156598/21.
DR	N-PSDB; ABK15577.


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AAW19704
ID AAW19704 standard; Protein; 332 AA.
XX
AC AAW19704;
XX
DT 19-AUG-1997 (first entry)
XX
DE Melanocortin-4 receptor.
XX
KW Melanocortin-3; MC3R; MC1R; MC2R; MC4R; MC5R; human; mouse; melanocyte;
KW pro-opiomelanocortin; adrenal cortical function; behaviour; learning;
KW memory; cardiovascular system; analgesia; thermoregulation; prolactin;
KW neurohumoral agent; biogenic amine.
XX
OS Homo sapiens.
XX
PN US5622860-A.
XX
PD 22-APR-1997.
XX
PF 17-FEB-1994; 94US-0200711.
XX
PR 17-FEB-1994; 94US-0200711.
XX
PA (UNMI ) UNIV MICHIGAN.
XX
PI Gantz I, Yamada T;
XX
DR WPI; 1997-244394/22.
DR N-PSDB; AAT68790.
XX
PT Nucleic acid molecules encoding melanocortin receptors - useful to
PT transfect mammalian cells lacking endogenous receptors to induce
PT their expression
XX
PS Claim 4; Column 43-46; 58pp; English.
XX
AAW19703-W19707 represent the human and mouse melanocortin (MC)
CC receptors. This sequence represents the MC4R, expressed primarily in
CC brain, but absent in the adrenal cortex, melanocytes and placenta. The
CC gene encoding this sequence is located at chromosome locus 18q21.3. MCs
CC are products of pro-opiomelanocortin post-translational processing, and
CC are known to have a broad array of physiological actions. MCs are known
CC to have effects on adrenal cortical functions and on melanocytes, as well
CC as affecting behaviour, learning, memory, control of the cardiovascular
CC system, analgesia, thermoregulation and the release of other neurohumoral
CC agents (such as prolactin and biogenic amines). The nucleic acids can be
CC used to transfect mammalian cells lacking endogenous MC receptors to
CC induce their expression. These sequences can also be used to screen and
CC identify drugs which specifically react with MCRs on the surface of a
CC cell. The drugs can then be used for treating diseases which have MCRs
CC implicated as one of their causes. Vectors containing these sequences can
CC also be used to treat the diseases.
XX
SQ Sequence 332 AA;
Query Match 96.0%; Score 1659.5; DB 18; Length 332;
Best Local Similarity 96.7%; Pred. No. 3.3e-174;
Matches 321; Conservative 5; Mismatches 5; Indels 1; Gaps 1;
QY 1 MNSTHHGHTSLHFNWNRSTYGPNSNASESLGKGYSDGCGYEQLFVSPVFTLGVISLL 60
DB 2 VNST-HRGMHTSLHLNWRSSYRLHNSNASESLGKGYSDGCGYEQLFVSPVFTLGVISLL 60
QY 61 ENILVIVIAKKNLHSPMTFFTCSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
DB 61 ENILVIVIAKKNLHSPMTFFTCSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
QY 121 IDNVDSVICSSLLASCSLLSTAVDRYFTIFALQYHNMTVRRVGIISCIWAACVTS 180
DB 121 IDNVDSVICSSLLASCSLLSTAVDRYFTIFALQYHNMTVRRVGIISCIWAACVTS 180
QY 181 GVLFIYSDSSAVIICLTMTFFTMLMASLYVHMFMLARLHKRIAVLPCTGTIRQGAN 240

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181 GILFIYSDSSAVIICLTMTFFTMLMASLYVHMFMLARLHKRIAVLPCTGTIRQGAN 240
241 MKGAIITLILIGVFWVCWAPFFLHLIFYISCPQNPYCVCFMSHENLYLILIMCNSIIDPL 300
241 MKGAIITLILIGVFWVCWAPFFLHLIFYISCPQNPYCVCFMSHENLYLILIMCNSIIDPL 300
301 IYALRSOELRKTKEIICCYPLGGICDLSSRY 332
301 IYALRSOELRKTKEIICCYPLGGICDLSSRY 332
RESULT 4
AAW79687
ID AAW79687 standard; Protein; 332 AA.
XX
AC AAW79687;
XX
DT 17-DEC-1998 (first entry)
XX
DE Melanocortin-4 receptor.
XX
KW Human melanocortin-4 receptor; MC4; MC1; MC3; therapeutic; brain;
KW adrenal cortex; melanocyte; placenta.
XX
OS Homo sapiens.
XX
PN US5817787-A.
XX
PD 06-OCT-1998.
XX
PF 23-APR-1997; 97US-0842045.
XX
PR 17-FEB-1994; 94US-0200711.
PR 27-JUN-1996; 96US-0672109.
PR 23-APR-1997; 97US-0842045.
XX
PA (UNMI ) UNIV MICHIGAN.
XX
PI Gantz I, Yamada T;
XX
DR WPI; 1998-556471/47.
DR N-PSDB; AAV62352.
XX
PT DNA encoding melanocortin-5 receptor - useful in hybridisation
PT assays for melanocortin-5 receptor nucleic acids
XX
PS Disclosure; Column 43-46; 58pp; English.
XX
The present sequence represents the human melanocortin-4 (MC4) receptor,
CC the gene of which has been localised to chromosome 18q21.3. This
CC receptor is activated by both the amino and carboxyl terminal end amino
CC acids of melanocortins and has been found to be expressed primarily in
CC the brain and is absent from the adrenal cortex, melanocytes and
CC placenta. The DNA sequence that produces this polypeptide was identified
CC by using oligonucleotides constructed from previously identified
CC receptors MC1 and MC3, this was performed by using these oligonucleotides
CC to search genomic DNA for other members of the receptor family. These
CC genes and their products may be used to provide therapeutic vehicles for
CC the treatment of processes involving the function of melanocortin
CC receptors.
XX
SQ Sequence 332 AA;
Query Match 96.0%; Score 1659.5; DB 19; Length 332;
Best Local Similarity 96.7%; Pred. No. 3.3e-174;
Matches 321; Conservative 5; Mismatches 5; Indels 1; Gaps 1;
QY 1 MNSTHHGHTSLHFNWNRSTYGPNSNASESLGKGYSDGCGYEQLFVSPVFTLGVISLL 60
DB 2 VNST-HRGMHTSLHLNWRSSYRLHNSNASESLGKGYSDGCGYEQLFVSPVFTLGVISLL 60
QY 61 ENILVIVIAKKNLHSPMTFFTCSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120

```

Db 61 ENILVTATAKNNLHSPMYFFICS LAVADMLVSVNSGSETIITLLNSTDTDAQSFTVN 120
QY 121 IDNVDSVICSSLLASICSLLSTAVDRYETIFVALQYHNIMTVRRVGGIIISCIIWAACVTS 180
Db 121 IDNVDSVICSSLLASICSLLSTAVDRYETIFVALQYHNIMTVRRVGGIIISCIIWAACVTS 180
QY 181 GVLFIYSDSSAVIICLTMTFMTLMALMASLYVHMFELMARLHKRIAVLPDGTGAIROGAN 240
Db 181 GILFIYSDSSAVIICLTMTFMTLMALMASLYVHMFELMARLHKRIAVLPDGTGAIROGAN 240
QY 241 MKGATITLTILIGVFWVWAPFELHLIFYISCPQNPYCVCFMSHFNLILIMCNSIIDPL 300
Db 241 MKGATITLTILIGVFWVWAPFELHLIFYISCPQNPYCVCFMSHFNLILIMCNSIIDPL 300
QY 301 IYALRSQELRKTFKEIICCYPLGGCLDLSRY 332
Db 301 IYALRSQELRKTFKEIICCYPLGGCLDLSRY 332

RESULT 5
AAW33724
ID AAW33724 standard; Protein; 332 AA.
AC AAW33724;
DT 30-APR-1998 (first entry)
DE Human melanocortin-4 (MC4) receptor.
KW Melanocortin receptor; ligand; MC4; human.
OS Homo sapiens.
PN US5703220-A.
PD 30-DEC-1997.
PF 27-JUN-1996; 96US-0671525.
PR 17-FEB-1994; 94US-0200711.
PR 27-JUN-1996; 96US-0671525.
PA (UNMI) UNIV MICHIGAN.
PI Gantz I, Yamada T;
PS WPI: 1998-076484/07.
DR N-PSDB; AAV06400.
XX DNA encoding human melanocortin-4 receptor - and cells useful in assay for MC4 receptor ligands
Claim 1; Columns 43-46; 59pp; English.

This is a human melanocortin receptor-4 (MC4). The MC4 receptor of this invention is activated by amino acids in the carboxyl and amino terminal portions of the heptapeptide sequence shared by all the melanocortin peptides. MC4 is expressed primarily in brain and is notably absent in the adrenal cortex, melanocytes and placenta. The MC4 receptor gene was localised to chromosome loci 18q21.3. The invention provides methods to identify ligands that bind to MC4 receptor.

Query Match 96.0%; Score 1659.5; DB 19; Length 332;
Best Local Similarity 96.7%; Pred. No. 3.3e-174;
Matches 321; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 MNSTHHGHMHTSLHFWNRSTYGPNSASESLGKGYSDGGYEQLFVSPFVTLGVISLL 60
Db 2 VNST-HRCMHTSLHLNRRSSYRLHNSASESLGKGYSDGGYEQLFVSPFVTLGVISLL 60

QY 61 ENILVTATAKNNLHSPMYFFICS LAVADMLVSVNSGSETIITLLNSTDTDAQSFTVN 120
Db 61 ENILVTATAKNNLHSPMYFFICS LAVADMLVSVNSGSETIITLLNSTDTDAQSFTVN 120
QY 121 IDNVDSVICSSLLASICSLLSTAVDRYETIFVALQYHNIMTVRRVGGIIISCIIWAACVTS 180
Db 121 IDNVDSVICSSLLASICSLLSTAVDRYETIFVALQYHNIMTVRRVGGIIISCIIWAACVTS 180
QY 181 GVLFIYSDSSAVIICLTMTFMTLMALMASLYVHMFELMARLHKRIAVLPDGTGAIROGAN 240
Db 181 GILFIYSDSSAVIICLTMTFMTLMALMASLYVHMFELMARLHKRIAVLPDGTGAIROGAN 240
QY 241 MKGATITLTILIGVFWVWAPFELHLIFYISCPQNPYCVCFMSHFNLILIMCNSIIDPL 300
Db 241 MKGATITLTILIGVFWVWAPFELHLIFYISCPQNPYCVCFMSHFNLILIMCNSIIDPL 300
QY 301 IYALRSQELRKTFKEIICCYPLGGCLDLSRY 332
Db 301 IYALRSQELRKTFKEIICCYPLGGCLDLSRY 332

RESULT 6
AAW92442
ID AAW92442 standard; Protein; 332 AA.
AC AAW92442;
DT 21-APR-1999 (first entry)
DE Human MC4 protein.
KW Melanocortin-4 receptor; MC1; MC2; MC3; MC4; MC5; detection; probe;
KW receptor binding; secondary signalling; tissue distribution.
OS Homo sapiens.

Key Location/Qualifiers
FT Protein 1..332 /note= "No stop codon given"
XX US5869257-A.
PN 09-FEB-1999.
PD 23-APR-1997; 97US-0842238.
PF 17-FEB-1994; 94US-0200711.
PR 27-JUN-1996; 96US-0671525.
PR 23-APR-1997; 97US-0842238.
XX (UNMI) UNIV MICHIGAN.
PI Gantz I, Yamada T;
XX WPI: 1999-152760/13.
DR N-PSDB; AAX01964.
XX Probe for detecting melanocortin-4 receptor genes - that specifically hybridises to defined DNA sequence
Example 1; Column 45-46; 60pp; English.

This sequence represents the human melanocortin-4 receptor, MC4. This protein is used in a method in which a nucleic acid probe useful for specifically detecting melanocortin-4 receptor genes is described. This probe is used to isolate genes encoding melanocortin receptors, to characterise melanocortin receptor binding and secondary signalling, and to determine tissue distribution of the melanocortin receptors.

Query Match 96.0%; Score 1659.5; DB 20; Length 332;
Best Local Similarity 96.7%; Pred. No. 3.3e-174;

Example 11; Page 71; 120pp; English.

New methods are described by which membrane polypeptides can be labelled. The method comprises chemoselective chemical ligation of the membrane polypeptide which is incorporated in a lipid matrix, and a ligation label. Both contain an amino acid having an unprotected reactive group that together undergo chemoselective ligation to form a covalent bond. The method can be used to label folded polypeptides embedded in a lipid membrane, by treating the polypeptide with a reagent that cleaves specifically adjacent to an amino acid with an unprotected reactive group and then ligating the cleaved polypeptide with the ligation label. The ligation label can be a chromophore, thus ligand binding to membrane bound polypeptides can be detected by contacting a membrane bound polypeptide comprising a chromophore, with the ligand under investigation and screening for binding in an assay characterized by detecting fluorescence resonance energy transfer (FRET) between the chromophore and a second chromophore. the chromophores comprising a donor and acceptor pair of a resonance energy transfer system. The methods are used for lipid matrix-assisted chemical ligation and synthesis of membrane polypeptides. Labeled membrane polypeptides are used to detect ligand binding and the identification of receptor domains, e.g. for structure/activity studies. They can also be used in drug screening, used for fluorescent resonance energy transfer (FRET) analysis of previously inaccessible membrane polypeptides. The method allows site-specific incorporation of labels during polypeptide synthesis and analysis of previously inaccessible membrane proteins. A Melanocortin receptor MC4 which also comprises a Factor Xa cleavage site (AAV83182) can be cleaved with Factor Xa to give a C-terminal alpha-thioester modified MC4 receptor ligation label (AAV83183) and an MC4 receptor membrane polypeptide cleavage product (AAV83184). Chemical ligation of cleaved MC4 in alternative membrane patches or micelles to an MC4 ligation label produces this synthetic labeled MC4 product (AAV83185).

Sequence 332 AA;

Query Match 96.0%; Score 1659.5; DB 21; Length 332;
Best Local Similarity 96.7%; Pred. No. 3.3e-174;
Matches 321; Conservative 5; Mismatches 5; Indels 1; Gaps 1;
QY 1 MNSTHHGHMTSLHFWNRSTYGPHSNASLSLCKGYSDGCGYBQLFVSPFVTLGVISLL 60
DB 2 VNST-HRGMHTSLHLWNRSYRLHNSASLSLCKGYSDGCGYBQLFVSPFVTLGVISLL 60
QY 61 ENILVIVATAKNKLNHSPMYFFICSLAVADMVLSVNSNGSETIVITLLNSTDTDAQSFTVN 120
DB 61 ENILVIVATAKNKLNHSPMYFFICSLAVADMVLSVNSNGSETIVITLLNSTDTDAQSFTVN 120
QY 121 IDNVDSVTCSSLLASICSLLSIADVDRYFTIFYALQYHNIMTVRRVGGIISCIWAACVTS 180
DB 121 IDNVDSVTCSSLLASICSLLSIADVDRYFTIFYALQYHNIMTVRRVGGIISCIWAACVTS 180
QY 181 GVLFIYSDSSAVIICLTIMFTMLMASLVHMFMLARLHKRIAVLPGGTGTROGAN 240
DB 181 GVLFIYSDSSAVIICLTIMFTMLMASLVHMFMLARLHKRIAVLPGGTGTROGAN 240
QY 241 MKGAILTLILIGVFFVVCWAPFELHLIFYSICPNQPCVCFMSHFNLYLLIMCNSIIDPL 300
DB 241 MKGAILTLILIGVFFVVCWAPFELHLIFYSICPNQPCVCFMSHFNLYLLIMCNSIIDPL 300
QY 301 IYALRSQELRKTFFKEIICCYPLGGICDLSRY 332
DB 301 IYALRSQELRKTFFKEIICCYPLGGICDLSRY 332

RESULT 9

AAB68490

ID AAB68490 standard; Protein; 332 AA.

XX AC AAB68490;

XX

DT

XX

DE

XX

KW

XX

KW

XX

KW

XX

KW

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OS

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XX

XX

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XX

PF

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PR

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PA

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23-JUL-2001 (first entry)

Amino acid sequence of a human melanocortin-4 receptor (MC-R4).

Human: melanocortin-4 receptor; MC-R4; transgenic animal; body weight;

food intake; obesity; diabetes; anorexia; cachexia; cancer;

sexual dysfunction; pain; impaired memory; neuronal regeneration;

neuropathy; growth disorder; growth hormone;

insulin-like growth factor-1.

Homo sapiens.

WO200133956-A1.

17-MAY-2001.

13-NOV-2000; 2000WO-US31061.

12-NOV-1999; 99US-0165074.

(MERI) MERCK & CO INC.

Van Der Ploeg LHT, Chen AS, Chen HY, Forrest MJ, MacIntyre DE;

Metzger JM, Palyha OC, Feighner SD, Hreniuk D;

N-PSDB; AAF85465.

WPI; 2001-343541/36.

New transgenic animal with non-functional gene for melanocortin-4

receptor, useful for identifying specific modulators, potentially used

for treating obesity or diabetes

Disclosure; Fig 2; 58pp; English.

The present sequence represents a human melanocortin-4 receptor (MC-R4).

The specification describes transgenic non-human animals whose somatic

and germ cells contain at least one non-functional gene for MC-4R

protein. The transgenic animals, or cells derived from them, are used

to screen for compounds that modulate MC-4R. These modulators are

potentially useful for regulating body weight and food intake and

treatment of associated diseases, obesity; diabetes; anorexia; cachexia;

cancer; sexual dysfunction; pain; impaired memory or neuronal

regeneration; neuropathy; growth disorders linked to growth hormone

and insulin-like growth factor-1. They can also be used to study MC-4R

expression and activity.

Query Match 96.0%; Score 1659.5; DB 22; Length 332;

Best Local Similarity 96.7%; Pred. No. 3.3e-174;

Matches 321; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 MNSTHHGHMTSLHFWNRSTYGPHSNASLSLCKGYSDGCGYBQLFVSPFVTLGVISLL 60

DB 2 VNST-HRGMHTSLHLWNRSYRLHNSASLSLCKGYSDGCGYBQLFVSPFVTLGVISLL 60

QY 61 ENILVIVATAKNKLNHSPMYFFICSLAVADMVLSVNSNGSETIVITLLNSTDTDAQSFTVN 120

DB 61 ENILVIVATAKNKLNHSPMYFFICSLAVADMVLSVNSNGSETIVITLLNSTDTDAQSFTVN 120

QY 121 IDNVDSVTCSSLLASICSLLSIADVDRYFTIFYALQYHNIMTVRRVGGIISCIWAACVTS 180

DB 121 IDNVDSVTCSSLLASICSLLSIADVDRYFTIFYALQYHNIMTVRRVGGIISCIWAACVTS 180

QY 181 GVLFIYSDSSAVIICLTIMFTMLMASLVHMFMLARLHKRIAVLPGGTGTROGAN 240

DB 181 GVLFIYSDSSAVIICLTIMFTMLMASLVHMFMLARLHKRIAVLPGGTGTROGAN 240

QY 241 MKGAILTLILIGVFFVVCWAPFELHLIFYSICPNQPCVCFMSHFNLYLLIMCNSIIDPL 300

DB 241 MKGAILTLILIGVFFVVCWAPFELHLIFYSICPNQPCVCFMSHFNLYLLIMCNSIIDPL 300

QY 301 IYALRSQELRKTFFKEIICCYPLGGICDLSRY 332

Db 121 IDNVDSVICSSLLASICSLLSIAVDRTYFIFYALQYHNIMTVKRVGISISCIWAACVTS 180
Qy 181 GVLFIYSDSSAVIICLTITMFTMALMASLYVHMFMLMARLHKRIKRIAVLPCTGTIROGAN 240
Db 181 GILFIYSDSSAVIICLTITMFTMALMASLYVHMFMLMARLHKRIKRIAVLPCTGTGTIROGAN 240
Qy 241 MKGAIITLILIGVFWVCWAPFELHIFVYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
Db 241 MKGKITLILIGVFWVCWAPFELHIFVYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
Qy 301 IYALRSQELRKTFKEIICCPYPLGGLDLSRY 332
Db 301 IYALRSQELRKTFKEIICCPYPLGGLDLSRY 332

RESULT 13
AA94301
ID AAY94301 standard; Protein; 332 AA.
AC AAY94301;
XX
XX
DT 04-AUG-2000 (first entry)
DE Rhesus monkey melanocortin-4 receptor protein.
XX Rhesus monkey; rhodopsin; G-protein coupled receptor; anorectic;
KW melanocyte stimulating hormone; melanocortin receptor; obesity.
XX Macaca mulatta.
XX WO200027863-A1.
XX 18-MAY-2000.
XX
XX 05-NOV-1999; 99WO-US25767.
XX
XX 09-NOV-1998; 98US-0107721.
XX (MERI) MERCK & CO INC.
XX MacNeil DJ, Weinberg DH, Van Der Ploeg LHT;
XX WPI; 2000-376480/32.
XX N-PSDB; AAA26972.
XX
XX Novel DNA encoding rhesus monkey melanocortin 4 receptor protein,
XX recombinant vectors and host cells, useful in methods for identifying
XX selective agonists and antagonists
XX
XX Claim 27; Page 35; 53pp; English.

The present sequence is the rhesus monkey melanocortin-4
receptor protein (MC-4R). Melanocortin receptors belong to the rhodopsin
sub-family of G-protein coupled receptors. They bind and are
activated by peptides such as alpha-, beta-, or gamma-melanocyte
stimulating hormones derived from the pro-opiomelanocortin gene and they
are believed to mediate a wide range of physiological functions.
The rhesus MC-4R gene was isolated by PCR using a series of four
oligonucleotides (AAA26973-A26976) based on the human MC-4R gene sequence
and designed to incorporate a restriction enzyme site for cloning into
the expression vector pCI-neo. The recombinant vector was transformed
into DH5a cells in preparation for DNA sequencing. The MC-4R gene
sequence (AAA26972) or a mutated form may be introduced into an
expression vector for expression in host cells. The subcellular
membrane fractions will comprise either wild-type or mutant forms of
rhesus MC-4R at enhanced levels and can be used in assays to identify
ligand binding, activators and modulators, agonists and antagonists of
MC-4R. This will allow for selection of compounds that are active for
the rhesus receptor in vitro and will allow the selection of novel
drugs to treat obesity.

Sequence 332 AA;

Query Match 95.2%; Score 1645.5; DB 21; Length 332;
Best Local Similarity 95.8%; Pred. No. 1.2e-172;
Matches 318; Conservative 6; Mismatches 7; Indels 1; Gaps 1;
Qy 1 MNSFHHGCHTSLHFWNRSTYGPHSNASESLGKGYSDGGCYEQLFVSPVFTLGVISLL 60
Db 2 VNST-HRGMHASLHLNRRSSHLHNSASESLGKGYSDGGCYEQLFVSPVFTLGVISLL 60
Qy 61 ENILVIVAIAKNNKLNHSPMYFFICSLAVADMVSVNSGSETIVITLLNSTDTDAQSFVN 120
Db 61 ENILVIVAIAKNNKLNHSPMYFFICSLAVADMVSVNSGSETIVITLLNSTDTDAQSFVN 120
Qy 121 IDNVDSVICSSLLASICSLLSIAVDRTYFIFYALQYHNIMTVKRVGIIISCIWAACVTS 180
Db 121 IDNVDSVICSSLLASICSLLSIAVDRTYFIFYALQYHNIMTVKRVGIIISCIWAACVTS 180
Qy 181 GVLFIYSDSSAVIICLTITMFTMALMASLYVHMFMLMARLHKRIKRIAVLPCTGTIROGAN 240
Db 181 GILFIYSDSSAVIICLTITMFTMALMASLYVHMFMLMARLHKRIKRIAVLPCTGTGTIROGAN 240
Qy 241 MKGAIITLILIGVFWVCWAPFELHIFVYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
Db 241 MKGAIITLILIGVFWVCWAPFELHIFVYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
Qy 301 IYALRSQELRKTFKEIICCPYPLGGLDLSRY 332
Db 301 IYALRSQELRKTFKEIICCPYPLGGLDLSRY 332

RESULT 14
AAY83182
ID AAY83182 standard; protein; 332 AA.
XX
XX AAY83182;
XX
DT 24-JUL-2000 (first entry)
DE Melanocortin receptor MC4 comprising Factor Xa cleavage site.
XX
XX Membrane polypeptide; lipid matrix; synthesis; ligation;
KW chemoselective ligation; fluorescence resonance energy transfer;
KW FRET; chromophore; ligand; receptor domain; drug screening;
KW diagnosis; ion channel; melanocortin receptor; MC4.
XX
XX Synthetic.
XX Homo sapiens.
XX WO200012536-A2.
XX
XX 09-MAR-2000.
XX
XX 26-AUG-1999; 99WO-US19542.
XX
XX 31-AUG-1998; 98US-0144964.
XX 05-MAR-1999; 99US-0263971.
XX
XX (GRYP) GRYPHON SCI.
XX
XX Kochendoerfer GG, Hunter CL, Kent SBH, Botti P;
XX WPI; 2000-270792/23.
XX
XX Selectively labeled membrane peptides, useful e.g. for detecting ligand
XX binding to receptors and in drug screening, are prepared, in lipid
XX matrix, by reaction between amino acid residues
XX
XX Example 11; Page 68-69; 120pp; English.

New methods are described by which membrane polypeptides can be
labelled. The method comprises chemoselective chemical ligation of
the membrane polypeptide which is incorporated in a lipid matrix,
and a ligation label. Both contain an amino acid having an
unprotected reactive group that together undergo chemoselective

Db 301 IYALRSOELRKTKEIICCYPLGGLCDLSSRY 332

Search completed: June 4, 2003, 18:15:42
Job time : 53 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 4, 2003, 17:58:11 ; Search time 12.5 Seconds
(without alignments)
781.473 Million cell updates/sec

Title: US-09-884-211a-3

Perfect score: 1728

Sequence: 1 MNSTHHGHMTSLHFWNRST.....FKRIICYPGGICLDSRY 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PCRU5_COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1659.5	96.0	332	1	US-08-671-525B-8
2	1659.5	96.0	332	1	US-08-672-109B-8
3	1659.5	96.0	332	2	US-08-842-045-8
4	1659.5	96.0	332	2	US-08-842-238-8
5	1659.5	96.0	332	2	US-08-780-749A-2
6	1659.5	96.0	332	3	US-08-629-335B-8
7	1659.5	96.0	332	4	US-08-870-511-2
8	1659.5	96.0	332	4	US-09-384-302A-9
9	1653.5	95.7	332	2	US-08-662-560-2
10	1653.5	95.7	332	2	US-08-780-749A-6
11	1653.5	95.7	332	4	US-08-870-511-6
12	1648.5	95.4	332	4	US-08-870-511-8
13	1647.5	95.3	332	4	US-08-870-511-10
14	1647.5	95.3	332	4	US-08-870-511-12
15	1632.5	94.5	332	4	US-09-384-302A-6
16	1613.5	93.4	332	3	US-08-706-281A-16
17	1613.5	93.4	332	4	US-09-097-231-16
18	1407	81.4	293	4	US-09-384-302A-8
19	1030	59.6	325	3	US-08-706-281A-18
20	1030	59.6	325	4	US-09-097-231-18
21	1027	59.4	325	1	US-08-671-525B-10
22	1027	59.4	325	1	US-08-672-109B-10
23	1027	59.4	325	2	US-08-842-045-10
24	1027	59.4	325	2	US-08-842-238-10
25	1027	59.4	325	3	US-08-629-335B-10
26	1004.5	58.1	325	4	US-08-387-805-16
27	987.5	57.1	360	1	US-08-671-525B-6

28	987.5	57.1	360	1	US-08-672-109B-6	Sequence 6, Appli
29	987.5	57.1	360	2	US-08-842-045-6	Sequence 6, Appli
30	987.5	57.1	360	2	US-08-842-238-6	Sequence 6, Appli
31	987.5	57.1	360	2	US-08-780-749A-1	Sequence 1, Appli
32	987.5	57.1	360	3	US-08-629-335B-6	Sequence 6, Appli
33	987.5	57.1	360	4	US-08-870-511-1	Sequence 1, Appli
34	971	56.2	323	2	US-08-044-812A-4	Sequence 4, Appli
35	971	56.2	323	2	US-08-475-637-4	Sequence 4, Appli
36	971	56.2	323	4	US-09-191-359-4	Sequence 4, Appli
37	967	56.0	323	3	US-08-706-281A-12	Sequence 12, Appli
38	967	56.0	323	4	US-09-097-231-12	Sequence 12, Appli
39	754.5	43.7	315	1	US-07-866-979-4	Sequence 4, Appli
40	754.5	43.7	315	2	US-08-466-906B-4	Sequence 4, Appli
41	754.5	43.7	315	3	US-08-706-281A-4	Sequence 4, Appli
42	754.5	43.7	315	4	US-09-201-746-4	Sequence 4, Appli
43	754.5	43.7	315	4	US-09-097-231-4	Sequence 4, Appli
44	752.5	43.5	317	4	US-08-387-805-2	Sequence 2, Appli
45	751.5	43.5	317	1	US-07-866-979-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-08-671-525B-8
; Sequence 8, Application US/08671525B
; Patent No. 5703220
; GENERAL INFORMATION:
; APPLICANT: Yamada, Tadataka
; APPLICANT: Gantz, Ira
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: US
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/671,525B
; FILING DATE: June 27, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, DeAnn F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-000853DVB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-671-525B-8

Query Match 96.0%; Score 1659.5; DB 1; Length 332;
Best Local Similarity 96.7%; Pred. No. 1.6e-125;
Matches 321; Conservative 5; Mismatches 5; Indels 1; Gaps 1;
Qy 1 MNSTHHGHMTSLHFWNRSTYGHPSNASESLGKGYSDGGCYEQLFVSPVFTLGVISLL 60
Db 2 VNST-HRGMHTSLHWNRSYSLHNSASESLGKGYSDGGCYEQLFVSPVFTLGVISLL 60
Qy 61 ENILVIVAIARNKLNHSPMYFFICSLAVADMVSVNSGSETIVITLLNSTDTDAQSFTVN 120
|||||

Db	61	ENTLVIVATAKKNKHLSPWFFICSLAVADMLVSVNGSETHIITLNLNSTDDAQGFTVN	120
Qy	121	IDNVDSVICSSLLASICSLLSIAVDRTFTFYALQYHNIMTVRRVGIIISCIIWAAC	180
Db	121	IDNVDSVICSSLLASICSLLSIAVDRTFTFYALQYHNIMTVRRVGIIISCIIWAAC	180
Qy	181	GVLFIIYDSSAVIICLTITMFTMLALMASLYVHMFMLARLHKRIAVLPGTGIROGAN	240
Db	181	GILFIIYDSSAVIICLTITMFTMLALMASLYVHMFMLARLHKRIAVLPGTGAIROGAN	240
Qy	241	MKGATLTILICGVVVCWAPFELHLIFYISCPQNPVCVCFMSHFNLYLIIMCNSIIDPL	300
Db	241	MKGATLTILICGVVVCWAPFELHLIFYISCPQNPVCVCFMSHFNLYLIIMCNSIIDPL	300
Qy	301	IYALRSQELRKTFKEIICCYPLGGCLDSRRY	332
Db	301	IYALRSQELRKTFKEIICCYPLGGCLDSRRY	332

RESULT 2

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US-08-672-109B-8
; Sequence 8, Application US/08672109B
; Patent No. 5710265
; GENERAL INFORMATION:
; APPLICANT: Yamada, Tadataka
; APPLICANT: Gantz, Ira
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: US
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672.109B
; FILING DATE: June 27, 1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, DeAnn F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-000853DVC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-672-109B-8

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Db	121	IDNVDSVICSSLLASICSLSIAVDRYFTIFYALQYHNIMTVKRVGIIISCIWAAC	180
Qy	181	GVLFIIYSDSSAVIICLLTTFMTLMALMASLVVHMFMLARHMKRIAVLP	240
Db	181	GILFIIYSDSSAVIICLLTTFMTLMALMASLVVHMFMLARHMKRIAVLP	240
Qy	241	MKGATTLTILIGVFVVCWAPFFLHFIYISCPQNPYCVCFMSHFNL	300
Db	241	MKGATTLTILIGVFVVCWAPFFLHFIYISCPQNPYCVCFMSHFNL	300
Qy	301	IYALRSQELRTFKETICCYPLGGCLDLSRRY	332
Db	301	IYALRSQELRTFKETICCYPLGGCLDLSRRY	332

RESULT. T 3

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RES001 3
US-08-842-045-8
: Sequence 8, Application US/08842045
: Patent No. 5817787
: GENERAL INFORMATION:
: APPLICANT: Yamada, Tadataka
: APPLICANT: Gantz, Ira
: TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
: NUMBER OF SEQUENCES: 23
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
: STREET: P.O. Box 828
: CITY: Bloomfield Hills
: STATE: MI
: COUNTRY: US
: ZIP: 48303
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/842,045
: FILING DATE:
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, Deann F.
: REGISTRATION NUMBER: 36683
: REFERENCE/DOCKET NUMBER: 2115-000853DVE
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (810)641-1600
: TELEFAX: (810)641-0270
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 332 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-842-045-8

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Query Match	96.0%	Score 1659, 5;	DB 1;	Length 332;
Best Local Similarity	96.7%	Pred. No. 1.6e-125;		
Matches 321;	Conservative 5;	Mismatches 5;	Indels 1;	Gaps 1
QY	1	MNSTHHGMHTSLHFWRNSTYGPHSNASESLGRGYDGGCYEQLFVSPVFFVLGVISLL	60	
Db				
	2	VNST-HRCGMHTSLHLNRRSSVRLHSNASESLGRGYDGGCYEQLFVSPVFFVLGVISLL	60	
QY	61	ENILVIVAIAKNNLHSPMYFFICSLAVADMLVSVNSGSETIITLLNSTDDAQSFTN	120	
Db	61	ENILVIVAIAKNNLHSPMYFFICSLAVADMLVSVNSGSETIITLLNSTDDAQSFTN	120	
QY	121	IDNVDSVICSSLASICSLSTAVDRYFFIFYALQYHNTMTRVRRVGLIISCIWAACTVS	180	

Db 181 GILFIYSDSAVILCIITMFTMALMASLYVHMFMLARLHKRIAVLPCTGAIRQAN 240
Qy 241 MKGAITITILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
Db 241 MKGAITITILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
Qy 301 IYALRSOELRKTKEIICCVPLGGLCDLSRY 332
Db 301 IYALRSOELRKTKEIICCVPLGGLCDLSRY 332

RESULT 4

US-08-842-238-8
; Sequence 8, Application US/08842238
; Patent No. 5869257
; GENERAL INFORMATION:
; APPLICANT: Yamada, Tadataka
; APPLICANT: Gantz, Ira
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: US
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842.238
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, DeAnn F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-000853DVD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-842-238-8

Query Match 96.0%; Score 1659.5; DB 2; Length 332;
Best Local Similarity 96.7%; Pred. No. 1.6e-125;
Matches 321; Conservative 5; Mismatches 5; Indels 1; Gaps 1;
Qy 1 MNSHHGMMTSLHFWNRSTYGHNSNASESLGKGYSDGCVYQQLFVSPVFTLGVISLL 60
Db 2 VNST-HRGMHTSLHNRSSYRLHNSNASESLGKGYSDGCVYQQLFVSPVFTLGVISLL 60
Qy 61 ENILVIVAIKNNKLNHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFVN 120
Db 61 ENILVIVAIKNNKLNHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFVN 120
Qy 121 IDNVDSVICSLLASCSLLSIAVDYRFTIFYALQYHNIMTVRVGIIISCIWAACVTS 180
Db 121 IDNVDSVICSLLASCSLLSIAVDYRFTIFYALQYHNIMTVRVGIIISCIWAACVTS 180
Qy 181 GVFLIYSDSAVILCIITMFTMALMASLYVHMFMLARLHKRIAVLPCTGTIRQAN 240
Db 181 GILFIYSDSAVILCIITMFTMALMASLYVHMFMLARLHKRIAVLPCTGTIRQAN 240
Qy 241 MKGAITITILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300

Db 241 MKGAITITILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
Qy 301 IYALRSOELRKTKEIICCVPLGGLCDLSRY 332
Db 301 IYALRSOELRKTKEIICCVPLGGLCDLSRY 332

RESULT 5

US-08-780-749A-2
; Sequence 2, Application US/08780749A
; Patent No. 5932779
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank
; APPLICANT: Huszar, Dennis
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS
; TITLE OF INVENTION: USEFUL IN THE REGULATION OF BODY WEIGHT
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780.749A
; FILING DATE: 08-JAN-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Laura A. Coruzzi
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-780-749A-2

Query Match 96.0%; Score 1659.5; DB 2; Length 332;
Best Local Similarity 96.7%; Pred. No. 1.6e-125;
Matches 321; Conservative 5; Mismatches 5; Indels 1; Gaps 1;
Qy 1 MNSHHGMMTSLHFWNRSTYGHNSNASESLGKGYSDGCVYQQLFVSPVFTLGVISLL 60
Db 2 VNST-HRGMHTSLHNRSSYRLHNSNASESLGKGYSDGCVYQQLFVSPVFTLGVISLL 60
Qy 61 ENILVIVAIKNNKLNHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFVN 120
Db 61 ENILVIVAIKNNKLNHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFVN 120
Qy 121 IDNVDSVICSLLASCSLLSIAVDYRFTIFYALQYHNIMTVRVGIIISCIWAACVTS 180
Db 121 IDNVDSVICSLLASCSLLSIAVDYRFTIFYALQYHNIMTVRVGIIISCIWAACVTS 180
Qy 181 GVFLIYSDSAVILCIITMFTMALMASLYVHMFMLARLHKRIAVLPCTGTIRQAN 240
Db 181 GILFIYSDSAVILCIITMFTMALMASLYVHMFMLARLHKRIAVLPCTGTIRQAN 240
Qy 241 MKGAITITILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300

Db 241 MKGATLTILIGVVFVVCWAPFFHLHLYFISCPQNPYCVCFMSHFNLYLILMNCNSIIDPL 300

QY 301 IYALRSQELRKTFKEIICCYPLGGCLDLSRY 332
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Db 301 IYALRSQELRKTFKEIICCYPLGGCLDLSRY 332

RESULT 6
US-08-629-335B-8
; Sequence 8, Application US/08629335B
; Patent No. 6117975
; GENERAL INFORMATION:
; APPLICANT: Yamada, Tadataka
; APPLICANT: Gantz, Ira
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: US
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/629,335B
; FILING DATE: July 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Deann F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-000853DVA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-629-335B-8

Query Match 96.0%; Score 1659.5; DB 3; Length 332;
Best Local Similarity 96.7%; Pred. No. 1.6e-125;
Matches 321; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 MNSTHHGMHTSLHFWNRSTYGPHSNASESLGKGYSDGGCYBOLFVSPFVTLGVISLL 60
:|||||

Db 2 VNST-HRGMHTSLHLNRSYRLHNSASESLGKGYSDGGCYBOLFVSPFVTLGVISLL 60
:|||||

QY 61 ENLIVATAKKNLHSPMYFFICSLAVADMLVSVNSGSETIITLLNSTDTDAQSFTVN 120
:|||||

Db 61 ENLIVATAKKNLHSPMYFFICSLAVADMLVSVNSGSETIITLLNSTDTDAQSFTVN 120
:|||||

QY 121 IDNVDSVCSLLASICSLLSIADVRYFTIFVALQYHNIMTVRRVGIISCIWAACVTS 180
:|||||

Db 121 IDNVDSVCSLLASICSLLSIADVRYFTIFVALQYHNIMTVRRVGIISCIWAACVTS 180
:|||||

QY 181 GVLFIYSDSSAVIICLTMTFMTLMALMASLVHMFMLARLHKRIAVLPGTGTIRQGAN 240
:|||||

Db 181 GILFIYSDSSAVIICLTMTFMTLMALMASLVHMFMLARLHKRIAVLPGTGTIRQGAN 240
:|||||

QY 241 MKGATLTILIGVVFVVCWAPFFHLHLYFISCPQNPYCVCFMSHFNLYLILMNCNSIIDPL 300
:|||||

Db 241 MKGATLTILIGVVFVVCWAPFFHLHLYFISCPQNPYCVCFMSHFNLYLILMNCNSIIDPL 300
:|||||

QY 301 IYALRSQELRKTFKEIICCYPLGGCLDLSRY 332
|||||

Db 301 IYALRSQELRKTFKEIICCYPLGGCLDLSRY 332

RESULT 8
US-09-384-302A-9
; Sequence 9, Application US/09384302A
; Patent No. 6451543
; GENERAL INFORMATION:
; APPLICANT: Kochendoerfer, Gerd G
; APPLICANT: Hunter, Christie L
; APPLICANT: Kent, Stephen B.H.
; APPLICANT: Botti, Paolo
; APPLICANT: Gryphon Sciences
; TITLE OF INVENTION: Lipid Matrix-Assisted Chemical Ligation and Synthesis
; FILE OF INVENTION: Of Membrane Polypeptides
; FILE REFERENCE: grfn-028/02WO
; CURRENT APPLICATION NUMBER: US/09/384,302A
; CURRENT FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: 09/144,964
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 09/263,971
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 30

Db 301 IYALRSQELRKTFKEIICCYPLGGCLDLSRY 332

RESULT 7
US-08-870-511-2
; Sequence 2, Application US/08870511
; Patent No. 6287763
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank
; APPLICANT: Huszar, Dennis
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE
; TITLE OF INVENTION: REGULATION OF BODY WEIGHT
; FILE REFERENCE: 7853-083
; CURRENT APPLICATION NUMBER: US/08/870,511
; CURRENT FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-870-511-2

Query Match 96.0%; Score 1659.5; DB 4; Length 332;
Best Local Similarity 96.7%; Pred. No. 1.6e-125;
Matches 321; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 MNSTHHGMHTSLHFWNRSTYGPHSNASESLGKGYSDGGCYBOLFVSPFVTLGVISLL 60
:|||||

Db 2 VNST-HRGMHTSLHLNRSYRLHNSASESLGKGYSDGGCYBOLFVSPFVTLGVISLL 60
:|||||

QY 61 ENLIVATAKKNLHSPMYFFICSLAVADMLVSVNSGSETIITLLNSTDTDAQSFTVN 120
:|||||

Db 61 ENLIVATAKKNLHSPMYFFICSLAVADMLVSVNSGSETIITLLNSTDTDAQSFTVN 120
:|||||

QY 121 IDNVDSVCSLLASICSLLSIADVRYFTIFVALQYHNIMTVRRVGIISCIWAACVTS 180
:|||||

Db 121 IDNVDSVCSLLASICSLLSIADVRYFTIFVALQYHNIMTVRRVGIISCIWAACVTS 180
:|||||

QY 181 GVLFIYSDSSAVIICLTMTFMTLMALMASLVHMFMLARLHKRIAVLPGTGTIRQGAN 240
:|||||

Db 181 GILFIYSDSSAVIICLTMTFMTLMALMASLVHMFMLARLHKRIAVLPGTGTIRQGAN 240
:|||||

QY 241 MKGATLTILIGVVFVVCWAPFFHLHLYFISCPQNPYCVCFMSHFNLYLILMNCNSIIDPL 300
:|||||

Db 241 MKGATLTILIGVVFVVCWAPFFHLHLYFISCPQNPYCVCFMSHFNLYLILMNCNSIIDPL 300
:|||||

QY 301 IYALRSQELRKTFKEIICCYPLGGCLDLSRY 332
|||||

Db 301 IYALRSQELRKTFKEIICCYPLGGCLDLSRY 332

RESULT 8
US-09-384-302A-9
; Sequence 9, Application US/09384302A
; Patent No. 6451543
; GENERAL INFORMATION:
; APPLICANT: Kochendoerfer, Gerd G
; APPLICANT: Hunter, Christie L
; APPLICANT: Kent, Stephen B.H.
; APPLICANT: Botti, Paolo
; APPLICANT: Gryphon Sciences
; TITLE OF INVENTION: Lipid Matrix-Assisted Chemical Ligation and Synthesis
; FILE OF INVENTION: Of Membrane Polypeptides
; FILE REFERENCE: grfn-028/02WO
; CURRENT APPLICATION NUMBER: US/09/384,302A
; CURRENT FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: 09/144,964
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 09/263,971
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-384-302A-9

Query Match 96.0%; Score 1659.5; DB 4; Length 332;
Best Local Similarity 96.7%; Pred. No. 1.6e-125;
Matches 321; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

Qy 1 MNSTHHGMHTSLHFWNRSTYGPNSNASESLGKGYSDGCGYEQLFVSPVFTLGVISLL 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2 VNST-HRGMHTSLHLNRRSSYRLHNSNASESLGKGYSDGCGYEQLFVSPVFTLGVISLL 60
61 ENILVIVAIKNNKLNHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSTVN 120
Db 61 ENILVIVAIKNNKLNHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSTVN 120
Qy 121 IDNVDSVICSLLASCSLSTIAVDRYFTTFYALQYHNMTVRRVGIISCIWAACVTS 180
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 IDNVDSVICSLLASCSLSTIAVDRYFTTFYALQYHNMTVRRVGIISCIWAACVTS 180
Qy 181 GVLFIIYSDSSAVIICLITMFTMLMASLYVHMFMLARLHKRIKRIAVLPGTGTIROGAN 240
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 GILFIIYSDSSAVIICLITMFTMLMASLYVHMFMLARLHKRIKRIAVLPGTGTIROGAN 240
Qy 241 MKGAIITLILIGVFWVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMCSIIIDPL 300
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 MKGAIITLILIGVFWVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMCSIIIDPL 300
Qy 301 IYALRSQELRKTKFKEIICCYPLGGLDLSRY 332
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Db 301 IYALRSQELRKTKFKEIICCYPLGGLDLSRY 332

RESULT 9
US-08-662-560-2
; Sequence 2, Application US/08662560
; Patent No. 590609
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank
; APPLICANT: Huszar, Dennis
; APPLICANT: Wei, Gu
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS
; TITLE OF INVENTION: USEFUL IN THE REGULATION OF BODY WEIGHT
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/662,560
; FILING DATE: 10-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-060
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-662-560-2

Query Match 95.7%; Score 1653.5; DB 2; Length 332;
Best Local Similarity 96.4%; Pred. No. 4.7e-125;
Matches 320; Conservative 5; Mismatches 6; Indels 1; Gaps 1;
Qy 1 MNSTHHGMHTSLHFWNRSTYGPNSNASESLGKGYSDGCGYEQLFVSPVFTLGVISLL 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2 VNST-HRGMHTSLHLNRRSSYRLHNSNASESLGKGYSDGCGYEQLFVSPVFTLGVISLL 60
61 ENILVIVAIKNNKLNHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSTVN 120
Db 61 ENILVIVAIKNNKLNHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSTVN 120
Qy 121 IDNVDSVICSLLASCSLSTIAVDRYFTTFYALQYHNMTVRRVGIISCIWAACVTS 180
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Db 121 IDNVDSVICSLLASCSLSTIAVDRYFTTFYALQYHNMTVRRVGIISCIWAACVTS 180
Qy 181 GVLFIIYSDSSAVIICLITMFTMLMASLYVHMFMLARLHKRIKRIAVLPGTGTIROGAN 240
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Db 181 GILFIIYSDSSAVIICLITMFTMLMASLYVHMFMLARLHKRIKRIAVLPGTGTIROGAN 240
Qy 241 MKGAIITLILIGVFWVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMCSIIIDPL 300
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Db 241 MKGAIITLILIGVFWVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMCSIIIDPL 300
Qy 301 IYALRSQELRKTKFKEIICCYPLGGLDLSRY 332
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 301 IYALRSQELRKTKFKEIICCYPLGGLDLSRY 332

RESULT 10
US-08-780-749A-6
; Sequence 6, Application US/08780749A
; Patent No. 5932779
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank
; APPLICANT: Huszar, Dennis
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS
; TITLE OF INVENTION: USEFUL IN THE REGULATION OF BODY WEIGHT
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,749A
; FILING DATE: 08-JAN-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Laura A. Coruzzi
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-064

Db 241 MKGATLTILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILNCNSIIDPL 300

QY 301 IYALRSQELRTFKETICCVPLGGCLDSLRY 332

Db 301 IYALRSQELRTFKETICCVPLGGCLDSLRY 332

Search completed: June 4, 2003, 18:03:56
Job time : 14 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 4, 2003, 18:03:01 ; Search time 31 Seconds
(without alignments)
1105.670 Million cell updates/sec

Title: US-09-884-211a-3

Perfect score: 1728

Sequence: 1 MNSTHHGMMHTSLHFWNRST.....FKELICYPGLGLDLSSRY 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1728	100.0	332	9	US-09-884-211A-3
2	1685	97.5	332	9	US-09-884-211A-4
3	1604	92.8	332	9	US-09-910-180-2
4	1004.5	58.1	325	12	US-10-052-545-16
5	1000.5	57.9	323	10	US-09-903-395-2
6	752.5	43.5	317	12	US-10-052-545-2
7	721	41.7	297	9	US-10-151-431-4
8	711	41.1	296	12	US-10-015-948-2
9	697	40.3	297	9	US-10-151-431-6
10	356.5	20.6	364	9	US-09-971-228-6
11	356.5	20.6	364	9	US-09-811-838-2
12	356.5	20.6	364	10	US-09-842-316-3
13	356.5	20.6	364	10	US-09-731-030A-15
14	356.5	20.6	364	12	US-10-037-616-20
15	328	19.0	104	12	US-10-052-545-10
16	327	18.9	102	12	US-10-052-545-8
17	325	18.8	382	10	US-09-969-711-2
18	324.5	18.8	381	9	US-10-024-494-28
19	324.5	18.8	381	10	US-09-827-937A-18

20	324.5	18.8	381	10	US-09-842-316-6	Sequence 6, Appli
21	324.5	18.8	381	10	US-09-731-030A-17	Sequence 17, Appl
22	324	18.8	341	9	US-09-971-228-13	Sequence 13, Appl
23	324	18.8	346	9	US-09-971-228-15	Sequence 15, Appl
24	324	18.8	362	10	US-09-993-844-8	Sequence 8, Appli
25	324	18.8	381	12	US-10-037-616-19	Sequence 19, Appl
26	324	18.8	382	9	US-09-971-228-5	Sequence 5, Appli
27	324	18.8	382	9	US-09-759-514-2	Sequence 2, Appli
28	316.5	18.3	330	10	US-09-845-720-2	Sequence 2, Appli
29	314.5	18.2	353	9	US-09-971-228-11	Sequence 11, Appl
30	314.5	18.2	353	9	US-09-811-838-6	Sequence 6, Appli
31	314.5	18.2	353	9	US-10-097-340-338	Sequence 338, App
32	314.5	18.2	353	10	US-09-842-316-4	Sequence 4, Appli
33	314.5	18.2	353	10	US-09-731-030A-16	Sequence 16, Appl
34	314.5	18.2	353	12	US-10-037-616-25	Sequence 25, Appl
35	312.5	18.1	321	9	US-10-146-065-2	Sequence 2, Appli
36	308.5	17.9	348	10	US-09-903-799-2	Sequence 2, Appli
37	305.5	17.7	354	10	US-09-879-225-2	Sequence 2, Appli
38	304.5	17.6	353	10	US-09-771-063-2	Sequence 2, Appli
39	304.5	17.6	353	10	US-09-771-063-4	Sequence 4, Appli
40	304.5	17.6	353	12	US-10-037-616-23	Sequence 23, Appl
41	304	17.6	352	9	US-10-084-507B-21	Sequence 21, Appl
42	303.5	17.6	124	12	US-10-052-545-12	Sequence 12, Appl
43	303.5	17.6	353	9	US-10-084-507B-22	Sequence 22, Appl
44	303.5	17.6	353	10	US-09-731-030A-19	Sequence 19, Appl
45	302.5	17.5	330	10	US-09-845-720-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-884-211a-3
; Sequence 3, Application US/09884211a
; Publication No. US20030032791A1
; GENERAL INFORMATION:
; APPLICANT: Alan et. al.
; TITLE OF INVENTION: NOVEL MELANOCORTIN-4 RECEPTOR SEQUENCES AND
; TITLE OF INVENTION: SCREENING ASSAYS TO IDENTIFY COMPOUNDS USEFUL
; TITLE OF INVENTION: IN REGULATING ANIMAL APETITE AND METABOLIC RATE
; FILE REFERENCE: PCL0743A
; CURRENT APPLICATION NUMBER: US/09/884,211a
; CURRENT FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 60/213,909
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Feline MC4R protein Sequence
US-09-884-211a-3

Query Match	100.0%	Score	1728;	DB	9;	Length	332;
Best Local Similarity	100.0%	Pred. No.	9.3e-148;				
Matches	332;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MNSTHHGMMHTSLHFWNRSTY	GPHSNASESLGKGYSDGGCYEQLFVSPVFTLGVISLL	60			
Db	1	MNSTHHGMMHTSLHFWNRSTY	GPHSNASESLGKGYSDGGCYEQLFVSPVFTLGVISLL	60			
Qy	61	ENILVIVAIAKNNKLNHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFVN	120				
Db	61	ENILVIVAIAKNNKLNHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFVN	120				
Qy	121	IDNVDSYICSSLLASICSLLSIAVDYFTTFYALQYHNIMTVRRVGIISCIWAACFVS	180				
Db	121	IDNVDSYICSSLLASICSLLSIAVDYFTTFYALQYHNIMTVRRVGIISCIWAACFVS	180				
Qy	181	GVLFIIYSDSAVVICLTIMFTTLMALMASLYVHMFMLMARLHRIKRIAVLPQTGTIRQGAN	240				
Db	181	GVLFIIYSDSAVVICLTIMFTTLMALMASLYVHMFMLMARLHRIKRIAVLPQTGTIRQGAN	240				

QY 241 MKGATITLILGVVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMCSIIDPL 300
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Db 241 MKGATITLILGVVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMCSIIDPL 300
QY 301 IYALRSQELRKTFKEIICCPYLGGLDLSRY 332
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Db 301 IYALRSQELRKTFKEIICCPYLGGLDLSRY 332

RESULT 2

US-09-884-211A-4
; Sequence 4, Application US/09884211A
; Publication No. US20030032791A1
; GENERAL INFORMATION:
; APPLICANT: Alan et. al.
; TITLE OF INVENTION: NOVEL MELANOCORTIN-4 RECEPTOR SEQUENCES AND
; SCREENING ASSAYS TO IDENTIFY COMPOUNDS USEFUL
; TITLE OF INVENTION: IN REGULATING ANIMAL APPETITE AND METABOLIC RATE
; FILE REFERENCE: PC10743A
; CURRENT APPLICATION NUMBER: US/09/884,211A
; PRIOR FILING DATE: 2000-06-26
; PRIOR FILING DATE: 60/213,909
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Canine MC4R protein Sequence
US-09-884-211A-4

Query Match 97.5%; Score 1685; DB 9; Length 332;
Best Local Similarity 97.6%; Pred. No. 6.9e-144;
Matches 324; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MNSTHHGMHTSLHFNWNRSTYGPHSNASLKGSDGCGYEQLFVSPFVTLGVISLL 60
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Db 1 MNSTLQHGHTSLHFNWNRSTYGPHSNASLKGSDGCGYEQLFVSPFVTLGVISLL 60
QY 61 ENLIVVAIAKNNKLNHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDDAQSFVN 120
Db 61 ENLIVVAIAKNNKLNHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDDAQSFVN 120
QY 121 IDNVDSVICSSLLASICSLLSIADVDYFTIFVALQYHNIMTVRRVGGIIISCIWAACVTS 180
Db 121 IDNVDSVICSSLLASICSLLSIADVDYFTIFVALQYHNIMTVRRVGGIIISCIWAACVTS 180
QY 181 GVLFIYSDSSAVIICLIITMFTMLMASLVYHMFMLARLHKRIAVLPGTGTIRQGAN 240
Db 181 GVLFIYSDSSAVIICLIITMFTMLMASLVYHMFMLARLHKRIAVLPGTGTIRQGAN 240
QY 241 MKGATITLILGVVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMCSIIDPL 300
Db 241 MKGATITLILGVVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMCSIIDPL 300
QY 301 IYALRSQELRKTFKEIICCPYLGGLDLSRY 332
Db 301 IYALRSQELRKTFKEIICCPYLGGLDLSRY 332

RESULT 3

US-09-910-180-2
; Sequence 2, Application US/09910180
; Publication No. US20030082678A1
; GENERAL INFORMATION:
; APPLICANT: Hsiung, Hansen
; APPLICANT: Smith, Dennis
; APPLICANT: Zhang, Xing-Yue
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING BODY WEIGHT IN BOVINE SPECIES
; FILE REFERENCE: P-12621
; CURRENT APPLICATION NUMBER: US/09/910,180
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Bovine
US-09-910-180-2
Query Match 92.8%; Score 1604; DB 9; Length 332;
Best Local Similarity 94.3%; Pred. No. 1.4e-136;
Matches 313; Conservative 6; Mismatches 13; Indels 0; Gaps 0;
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Db 1 MNSTQPLGMHTSLHFNWNRSAHGMPTNVSESLAKGSDGCGYEQLFVSPFVTLGVISLL 60
QY 61 ENLIVVAIAKNNKLNHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDDAQSFVN 120
Db 61 ENLIVVAIAKNNKLNHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDDAQSFVN 120
QY 121 IDNVDSVICSSLLASICSLLSIADVDYFTIFVALQYHNIMTVRRVGGIIISCIWAACVTS 180
Db 121 IDNVDSVICSSLLASICSLLSIADVDYFTIFVALQYHNIMTVRRVGGIIISCIWAACVTS 180
QY 181 GVLFIYSDSSAVIICLIITMFTMLMASLVYHMFMLARLHKRIAVLPGTGTIRQGAN 240
Db 181 GVLFIYSDSSAVIICLIITMFTMLMASLVYHMFMLARLHKRIAVLPGTGTIRQGAN 240
QY 241 MKGATITLILGVVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMCSIIDPL 300
Db 241 MKGATITLILGVVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMCSIIDPL 300
QY 301 IYALRSQELRKTFKEIICCPYLGGLDLSRY 332
Db 301 IYALRSQELRKTFKEIICCPYLGGLDLSRY 332

RESULT 4

US-10-052-545-16
; Sequence 16, Application US/10052545
; Patent No. US20020142392A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Melanocyte stimulating hormone receptor
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/052,545
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/387,805
; FILING DATE: 21-FEB-95
; APPLICATION NUMBER: PCT/DK93/00273
; FILING DATE: 20-AUG-93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 1046/92
; FILING DATE: 21-AUG-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 1118/92
; FILING DATE: 10-SEP-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0528/93


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Query Match      43.5%; Score 752.5; DB 12; Length 317;
Best Local Similarity 51.2%; Pred. No. 5.7e-60;
Matches 152; Conservative 51; Mismatches 89; Indels 5; Gaps 4;

QY 27 ASSESLGKGYSDGG--CYEQLFVSPFVETLGVISLLENILVIVAIKNNKLNHSPMYFFIC 84
Db 20 AIFOLGLAANQTCARGCLE-VSISDGLFSLGLSVLENALVWATIAKNNRNHSPMYCFIC 78
QY 85 SLAVADMLVSVNGSETIVITLLNSTDTDAQSFTV-NIDNVDSVICSSLLASICSLLSI 143
Db 79 CLALSDLLVSGSNVLETAVILLLEAGALVARAAVLOQLDNVDIVTCSSMLSLCFLGAI 138
QY 144 ADVRYTIFVALQYHNIMTVRRVGGIIISCIWAACVSGVLFIYSDSSAVIICLIMFTT 203
Db 139 ADVRYISIFVALYHSHVITLPRARRRVAALVWASVVFTLFIAYDHRVALLCLVVFFLA 198
QY 204 MLALMASLYVHMFELMARLHKRTAVL-PGTGTTIROGANKMGATLTLILGVFVVCWAPFF 262
Db 199 MCLVMAVLYVHMLARACQAQGHARKRQRPVHOGFGLKGAVTLTLILGIFLCLWGPF 258
QY 263 LHIFYISCPQNPYCVCFMSHFNLYLILMCNSIIDPLIYALRSOELRKTEKRIICC 319
Db 259 LHLTLVLCPEHEHTCCICFKNFNFLALILICNAIIDPLIYAFHSQELRRTLKEVLTC 315

RESULT 7
US-10-151-431-4
; Sequence 4, Application US/10151431
; Publication No. US20030044973A1
; GENERAL INFORMATION:
; APPLICANT: Cone, Roger D
; Mountjoy, Kathleen G
; TITLE OF INVENTION: Mammalian Adrenocorticotrophic Hormone
; Receptors and Uses
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Allegrretti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/151,431
; FILING DATE: 20-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,298
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/866,560
; FILING DATE: 10-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20030044973A1nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 297 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-151-431-4

Query Match      41.7%; Score 721; DB 9; Length 297;
Best Local Similarity 46.1%; Pred. No. 3.6e-57;
Matches 142; Conservative 58; Mismatches 90; Indels 18; Gaps 3;

QY 26 NASESLGKGYSDGGCYEQLFVSPFVETLGVISLLENILVIVAIKNNKLNHSPMYFFICS 85
Db 6 NSYENINNTARNNSDCPRVLPPEIEIFTISVGVLENILVLLAVFKNKNLQAPMYFFICS 65
QY 86 LAVADMLVSVNGSETIVITLLNSTDTDAQ-SFTVNIDNVDSVICSSLLASICSLLSIA 144
Db 66 LAISDMLGSLYKILENILLILRNMGYLKPRGSFETADDIISLVLISLGSIFSLSVIA 125
QY 145 VDRYTFIFVALQYHNIMTVRRVGGIIISCIWAACVSGVLFIYSDSSAVIICLIMFTT 204
Db 126 ADRYITIFHALRYHSHVITMRTTWWLTVIWTCTGTGTTWIFSHHVPVITFTSLFPLM 185
QY 205 LALMASLYVHMFELMARLHKRTAVLPGTGTIROGANKMGATLTLILGVFVVCWAPFFLH 264
Db 186 LVFILCLYVHMFELMARSHTRKISTLP-----RANMKGAITLTLILGVFIFCWAPFVLH 238
QY 265 LHIFYISCPQNPYCVCFMSHFNLYLILMCNSIIDPLIYALRSOELRKTEKRIICCYPPLGG 324
Db 239 VLLMTFCPSNPYCAVMSLFQVNGMLMCNAVIDPIYAFRSPDELDAFKKMFEC----- 293
QY 325 LCDLSSRY 332
Db 294 -----SRY 296

RESULT 8
US-10-015-948-2
; Sequence 2, Application US/10015948
; Patent No. US20020133843A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; APPLICANT: Matthews, William
; APPLICANT: Moore, Mark
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING
; ADRENOCORTICOTROPIN HORMONE RECEPTOR GENE DISRUPTIONS
; FILE REFERENCE: R-605
; CURRENT APPLICATION NUMBER: US/10/015,948
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 60/254,906
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/324,583
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-015-948-2

Query Match      41.1%; Score 711; DB 12; Length 296;
Best Local Similarity 50.7%; Pred. No. 2.9e-56;
Matches 138; Conservative 47; Mismatches 79; Indels 8; Gaps 2;

QY 49 EVFVTLGVISLLENILVIVAIKNNKLNHSPMYFFICTSLAVADMLVSVNGSETIVITLLN 108
Db 29 EIFFTISVIGILENIVLLAVIKNNLQSPMYFFICTSLAISDMLGSLYKILENILLIFRN 88
QY 109 STDTDQAQ-SFTVNIDNVDSVICSSLLASICSLLSIAVDVRYTFIFVALQYHNIMTVRRVG 167
Db 89 MGYLPRGSFETADDIIDCMFILSLGSIFSLSVIAADRYITIFHALQYHSIVTMRRTI 148
QY 168 IISCIWAACVSGVLFIYSDSSAVIICLIMFTTLMALMASLYVHMFELMARLHKRIA 227
Db 149 ITLTIWMECTGSGITWIFSHHITVLTFTSLFPLMLVFIICLYIHMFELLARSHARKIS 208
QY 228 VLPGTGTIROGANKMGATLTLILGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLY 287
Db 209 TLPRT-----NMKGAMTLTLILGVFIFCWAPFVLHVLMLTFCPNPNPYCVCMISLQVFN 261
```


Db 189 ICDIENSNAPLYSDSYLFWAIFNL--VTFVVMVLYAHIFGYVRQRTMRMS-RHSSG 245
Qy 234 TIROGANNKGAI-TLTILIGVVFVVCWAPFHLHIFLYISCPQNPVCV-FMSHFNLXLILI 291
Db 246 PRNRDPTMSLLKTVVILGAFICWTPGLVLLLDVCCFQ-----CDVLAYERFFLLLA 300
Qy 292 MCNSIIDPLIYALRSQBLKTFKEIICC 319
Db 301 EFNSAMNPIIYSYRDKEMSATFRQILCC 328

RESULT 14

US-10-037-616-20
; Sequence 20, Application US/10037616
; Patent No. US20020123148A1
; GENERAL INFORMATION:
; APPLICANT: English, Denis
; APPLICANT: Kovacs, Richard J.
; APPLICANT: Rizzo, Maria T.
; APPLICANT: Sliva, Daniel T.
; TITLE OF INVENTION: Sphingolipid Compositions and Methods for Their Therapeutic Use
; FILE REFERENCE: 7042-119
; CURRENT APPLICATION NUMBER: US/10/037,616
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/243,887
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-037-616-20

Query Match 20.6%; Score 356.5; DB 12; Length 364;
Best Local Similarity 28.4%; Pred. No. 3e-24;
Matches 93; Conservative 65; Mismatches 115; Indels 55; Gaps 11;
Qy 15 FWRSTYGPHS---NASESIGKGYSDGCGYEQLFVSPEVFTLVGLVISLLENILVIVVIA 70
Db 33 FYNRS--GKHLATEWNTVSKLVMLG-----ITVCIFIMLANLLVMVAYI 75
Qy 71 KKNLHSPMYFFIGSLAVADMLVSVNSGSETIVITLNLSTDTAQSFVNIDNVISVIC 130
Db 76 VNRFEPIIYLYMANLAADFFAGLA-----FYLMFNTGPNTRRTVSTWLLRQGLID 129
Qy 131 SSLASTCSLLSTAVDRYFTFYALQYHNIMTVRRVGGIISCIWAACVTSVG----- 182
Db 130 TSLTASVANLLATAIERHITVF-RMQLHTRMSNRVWVVIWITMAIVMGAIPSVGWCNC 188
Qy 183 -----LFIIYSDSSAVTICLTMTFFTMALMASLYVHMFMLMARLHKRIAVLPCTG 233
Db 189 ICDIENSNAPLYSDSYLFWAIFNL--VTFVVMVLYAHIFGYVRQRTMRMS-RHSSG 245
Qy 234 TIROGANNKGAI-TLTILIGVVFVVCWAPFHLHIFLYISCPQNPVCV-FMSHFNLXLILI 291
Db 246 PRNRDPTMSLLKTVVILGAFICWTPGLVLLLDVCCFQ-----CDVLAYERFFLLLA 300
Qy 292 MCNSIIDPLIYALRSQBLKTFKEIICC 319
Db 301 EFNSAMNPIIYSYRDKEMSATFRQILCC 328

RESULT 15

US-10-052-545-10
; Sequence 10, Application US/10052545
; Patent No. US20020142392A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Melanocyte stimulating hormone receptor
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/052,545
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/387,805
; FILING DATE: 21-FEB-95
; APPLICATION NUMBER: PCT/DK93/00273
; FILING DATE: 20-AUG-93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 1046/92;
; FILING DATE: 21-AUG-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 1118/92;
; FILING DATE: 10-SEP-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0528/93;
; FILING DATE: 05-MAY-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 1102.0160000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; US-10-052-545-10

Query Match 19.0%; Score 328; DB 12; Length 104;
Best Local Similarity 60.6%; Pred. No. 2.5e-22;
Matches 63; Conservative 17; Mismatches 22; Indels 2; Gaps 1;

Qy 152 FYALQYHNIMTVRRVGGIISCIWAACVTSVGLFIYSDSSAVIICLTITMFFTMLMASL 211
Db 1 FYALRYHSIVTVRRALTLIVAIWCCVCGVVFVYSEKMWIVCLITMFFAMLLMGTL 60
Qy 212 YVHFMFLMARLHKRIAVLPCTGT--RQGANMKGAITLTILIGV 253
Db 61 YVHFMFLPARLHVKRIALPPADGVAPQOHSCKMGAVTITLLGI 104

Search completed: June 4, 2003, 18:13:53
Job time : 32 secs

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OM protein - protein search, using sw model

Run on: June 4, 2003, 18:12:51 ; Search time 26 Seconds

(without alignments)
1227.563 Million cell updates/sec

Title: US-09-884-211a-3

Perfect score: 1728

Sequence: 1 MNSTHHGMHTSLHFNWNRST.....FKRIICYPGLGLDLSRY 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1653.5	95.7	332	2 A57055	melanocortin recep
2	1074	62.2	215	2 B57055	melanocortin-4 rec
3	1047	60.6	325	2 JC2193	melanocortin recep
4	1027	59.4	372	2 I49008	melanocortin-5 rec
5	1023.5	59.2	325	2 JC5592	melanocortin 5 rec
6	1004.5	58.1	325	2 JN0764	melanocortin recep
7	1000.5	57.9	323	2 S43850	melanocortin 3 rec
8	993.5	57.5	360	2 B46647	melanocortin recep
9	971	56.2	323	2 S36636	melanocortin recep
10	965.5	55.9	325	2 I46416	melanocyte-stimula
11	832.5	48.2	314	2 S71420	melanocortin 1 rec
12	819.5	47.4	314	2 S70005	melanocortin 1 rec
13	773.5	44.8	317	2 S45708	MSH receptor - bov
14	763	44.2	317	2 T12055	melanocyte stimula
15	754.5	43.7	315	2 S25581	melanocyte-stimula
16	751.5	43.5	317	2 S29204	melanotropin recep
17	721	41.7	297	2 S42767	adrenocorticotropi
18	721	41.7	297	2 C43265	adrenocorticotropi
19	711	41.1	296	2 I52326	adrenocorticotropi
20	708	41.0	296	2 JC4046	adrenocorticotropi
21	697	40.3	297	2 I45849	gene ACTH receptor
22	356.5	20.6	364	2 JC5293	lysophosphatidic a
23	328.5	19.0	383	2 I53870	Edg-1 orphan recep
24	324.5	18.8	381	2 A35300	G protein-coupled
25	323	18.7	362	2 JC7559	spingosine 1-phos
26	322	18.6	317	2 JC2335	melanocortin recep
27	316.5	18.3	330	2 A55689	G protein-coupled
28	304	17.6	352	2 JC1465	probable G protein
29	302.5	17.5	330	2 S40454	G protein-coupled

ALIGNMENTS

RESULT 1

A57055

melanocortin receptor 4 - human

C:Species: Homo sapiens (man)

C:Date: 03-Oct-1995 #sequence_revision.03-Oct-1995 #text_change 24-Sep-1999

C:Accession: A57055; A47111

R:Mountjoy, K.G.; Mortrud, M.T.; Low, M.J.; Simerly, R.B.; Cone, R.D.

Mol. Endocrinol. 8, 1298-1308, 1994

A:Title: Localization of the melanocortin-4 receptor (MC4-R) in neuroendocrine and au

A:Reference number: A57055; MUID:95157557; PMID:7854347

A:Accession: A57055

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-332 <MOU>

A:Cross-references: GB:S77415; NID:g998456; PIDN:AA33341.1; PID:g998457

R:Gantz, I.; Miwa, H.; Konda, Y.; Shimoto, Y.; Tashiro, T.; Watson, S.J.; Delvalle, J

J. Biol. Chem. 268, 15174-15179, 1993

A:Title: Molecular cloning, expression, and gene localization of a fourth melanocorti

A:Reference number: A47111; MUID:93315499; PMID:8392067

A:Accession: A47111

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-168, '1', 170-332 <GAN>

A:Cross-references: GB:L08603; NID:g291977; PIDN:AAA35791.1; PID:g291978

C:Genetics:

A:Gene: GDB:MC4R

A:Cross-references: GDB:203939; OMIM:155541

A:Map position: 20q13.2-20q13.3

C:Superfamily: melanocortin receptor

C:Keywords: hormone receptor

Query Match 95.7%; Score 1653.5; DB 2; Length 332;
Best Local Similarity 96.4%; Pred. No. 9.9e-128;

Matches 320; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

Qy 1 MNSTHHGMHTSLHFNWNRSTYGPHSNASESLGKGYSDGGCYEQLFVSPVEVFTLGVISLL 60

Db 2 VNST-HRGMHTSLHLNKRSSYRLHSNASESLGKGYSDGGCYEQLFVSPVEVFTLGVISLL 60

Qy 61 ENILVIVAIAKNKLNHSPMYFFICSLAVADMLVSVNSGSEITVITLLNSTDTDAQSFVN 120

Db 61 ENILVIVAIAKNKLNHSPMYFFICSLAVADMLVSVNSGSEITVITLLNSTDTDAQSFVN 120

Qy 121 IDNVDSVYCSSLASICSLLSIAVDYFTTFYALQYHNIMTVRRVGIITIIICINAACTVS 180

Db 121 IDNVDSVYCSSLASICSLLSIAVDYFTTFYALQYHNIMTVRRVGIITIIICINAACTVS 180

Qy 181 GVLFIYSDSSAVIICLITMFTMALMASLYVHMFMLMARHUKRIKRIAVLPOTGTIRQGAN 240

Db 181 GILFIYSDSSAVIICLITMFTMALMASLYVHMFMLMARHUKRIKRIAVLPOTGTIRQGAN 240

Qy 241 MKGAITLTILIGVFVVCWAPFFLHIFVISCQPNPCVCFMSHENLYLILIMCNSIIDPL 300

Db 241 MKGATITLLIGVYVVCWAPFFLHLFIYISCPQNYCVCFMSHFNLYLILMCNSIIDPL 300
|||||

QY 301 IVALRSQELRKTKEIICCPYLGGLDLSRY 332
|||||

Db 301 IVALRSQELRKTKEIICCPYLGGLDLSRY 332
|||||

RESULT 2

B57055
melanocortin-4 receptor - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 07-May-1999
C:Accession: B57055
R:Mountjoy, K.G.; Trudrud, M.T.; Low, M.J.; Simerly, R.B.; Cone, R.D.
Mol. Endocrinol. 8, 1298-1308, 1994
A:Title: Localization of the melanocortin-4 receptor (MC4-R) in neuroendocrine and autonomic nervous system of the rat.
A:Reference number: A57055; MUID:95157557; PMID:7854347
A:Accession: B57055
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-215 <MUID>
C:Superfamily: melanocortin receptor

Query Match 62.2%; Score 1074; DB 2; Length 215;
Best Local Similarity 97.2%; Pred. No. 1.4e-80;
Matches 209; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 78 PMYFFICSLAVADMLVSVNGSETIVITLLNSTDDAQSFVNIDNVIDSVICSSLLASI 137
|||||

Db 1 PMYFFICSLAVADMLVSVNGSETIVITLLNSTDDAQSFVNIDNVIDSVICSSLLASI 60
|||||

QY 138 CSLLSIAVDRYTFIFALQYHNMVRRVGGIISCIWAACVSGVLIYDSSSAVIICL 197
|||||

Db 61 CSLLSIAVDRYTFIFALQYHNMVRRVGGIISCIWAACVSGVLIYDSSSAVIICL 120
|||||

QY 198 ITMFFTMLALMASLYVHFMFLMARLHKRIAVLPGTGTIROGANKGAILTLILIGVYVVC 257
|||||

Db 121 ITMFFTMLALMASLYVHFMFLMARLHKRIAVLPGTGTIROGANKGAILTLILIGVYVVC 180
|||||

QY 258 WAPFLLHLFIYISCPQNYCVCFMSHFNLYLILIM 292
|||||

Db 181 WAPFLLHLFIYISCPQNYCVCFMSHFNLYLILIM 215
|||||

RESULT 3

JC2193
melanocortin receptor, MC5 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 24-Sep-1999
C:Accession: JC2193
R:Griffon, N.; Mignon, V.; Facchinetti, P.; Diaz, J.; Schwartz, J.C.; Sokoloff, P.
Biochem. Biophys. Res. Commun. 200, 1007-1014, 1994
A:Title: Molecular cloning and characterization of the rat fifth melanocortin receptor.
A:Reference number: JC2193; MUID:94234987; PMID:8179577
A:Accession: JC2193
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-325 <GRI>
A:Cross-references: GB:L27081; NID:9435606; PIDN:AAA1577.1; PID:9435607
C:Superfamily: melanocortin receptor
C:Keywords: G protein-coupled receptor; receptor; transmembrane protein
F:37-63/Domain: transmembrane #status predicted <TM1>
F:73-98/Domain: transmembrane #status predicted <TM2>
F:117-138/Domain: transmembrane #status predicted <TM3>
F:159-179/Domain: transmembrane #status predicted <TM4>
F:193-211/Domain: transmembrane #status predicted <TM5>
F:240-263/Domain: transmembrane #status predicted <TM6>
F:276-297/Domain: transmembrane #status predicted <TM7>

Query Match 60.6%; Score 1047; DB 2; Length 325;
Best Local Similarity 65.0%; Pred. No. 3.4e-78;
Matches 202; Conservative 46; Mismatches 59; Indels 4; Gaps 3;

QY 26 NASES--LGKGYSD--GGCYEQLFVSPVFTLGVISLLENILVIVAIAKNKNLHSPMYFF 82
|||||

Db 15 NASEDNILQNNYNNKSSACEDMGIAVEVFLTLGLVSLLENILVIVAIAKNKNLHSPMYFF 74
|||||

QY 83 ICSLAVADMLVSVNGSETIVITLLNSTD--TDAQSFVNIDNVIDSVICSSLLASTCSLL 141
:|||||

Db 75 VGS LAVADMLVSVNGSETIVITLLNSTD--TDAQSFVNIDNVIDSVICSSLLASTCSLL 134
:|||||

QY 142 STAVDRYTFIFALQYHNMVRRVGGIISCIWAACVSGVLIYDSSSAVIICLITMF 201
:|||||

Db 135 ATAVDRYTFIFALQYHNMVRRVGGIISCIWAACVSGVLIYDSSSAVIICLITMF 194
:|||||

QY 202 FTMLALMASLYVHFMFLMARLHKRIAVLPGTGTIROGANKGAILTLILIGVYVVCWAPF 261
|||||

Db 195 FTMLALMASLYVHFMFLMARLHKRIAVLPGTGTIROGANKGAILTLILIGVYVVCWAPF 254
|||||

QY 262 FTMLALMASLYVHFMFLMARLHKRIAVLPGTGTIROGANKGAILTLILIGVYVVCWAPF 321
|||||

Db 255 FTMLALMASLYVHFMFLMARLHKRIAVLPGTGTIROGANKGAILTLILIGVYVVCWAPF 314
|||||

QY 322 LGGLCDLSRY 332
|||||

Db 315 FRRTCTLLGRY 325
|||||

RESULT 4

I49008
melanocortin-5 receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C:Accession: I49008; A54245; JC2244
R:Pathi, Z.; Iben, L.G.; Parker, E.M.
Neurochem. Res. 20, 107-113, 1995
A:Title: Cloning, expression, and tissue distribution of a fifth melanocortin receptor.
A:Reference number: I49008; MUID:95258173; PMID:7739752
A:Accession: I49008
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-372 <RES>
A:Cross-references: EMBL:U08354; NID:9522165; PIDN:AAA76585.1; PID:9522166
R:Labbe, O.; Desarnaud, F.; Eggerickx, D.; Vassart, G.; Parmentier, M.
Biochemistry 33, 4543-4549, 1994
A:Title: Molecular cloning of a mouse melanocortin 5 receptor gene widely expressed in the brain.
A:Reference number: A54245; MUID:94213827; PMID:8161509
A:Accession: A54245
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 48-120, F', 122-372 <LAB>
A:Cross-references: GB:X76295; NID:9498973; PIDN:CAA53943.1; PID:9498974
A:Experimental source: clone HGMP01B
A:Note: sequence extracted from NCBI backbone (NCBIP:145988)
R:Gantz, I.; Shimoto, Y.; Konda, Y.; Miwa, H.; Dickinson, C.J.; Yamada, T.
Biochem. Biophys. Res. Commun. 200, 1214-1220, 1994
A:Title: Molecular cloning, expression, and characterization of a fifth melanocortin receptor.
A:Reference number: JC2244; MUID:94241974; PMID:8185570
A:Accession: JC2244
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 48-372 <GAN>
A:Cross-references: GB:L22527; NID:9468377; PIDN:AAA21337.1; PID:9468378
C:Superfamily: melanocortin receptor
C:Keywords: receptor; transmembrane protein
F:84-109/Domain: transmembrane #status predicted <TM1>
F:121-144/Domain: transmembrane #status predicted <TM2>
F:164-185/Domain: transmembrane #status predicted <TM3>
F:206-226/Domain: transmembrane #status predicted <TM4>
F:232-257/Domain: transmembrane #status predicted <TM5>
F:287-310/Domain: transmembrane #status predicted <TM6>
F:324-344/Domain: transmembrane #status predicted <TM7>

Query Match 59.4%; Score 1027; DB 2; Length 372;
Best Local Similarity 64.0%; Pred. No. 1.7e-76;
Matches 199; Conservative 46; Mismatches 62; Indels 4; Gaps 3;

[illegible]

RESULT 9

S36636

melanocortin receptor 3 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 02-Jun-2000

C:Accession: A48254; S36636

R:Roselli-Rehfuess, L.; Mountjoy, K.G.; Robbins, L.S.; Mortrud, M.T.; Low, M.J.; Tatro

Proc. Natl. Acad. Sci. U.S.A. 90, 8856-8860, 1993

A:Title: Identification of a receptor for gamma melanotropin and other proopiomelanoc

A:Reference number: A48254; MUID:94022273; PMID:8415620

A:Accession: A48254

A>Status: preliminary; translated from GB/EMBL/DBDB

A:Molecule type: mRNA

A:Residues: 1-323 <ROS>

A:Cross-references: EMBL:X70667; NID:X396551; PIDN:CAA50005.1; PID:g396552

A:Note: submitted to the EMBL Data Library, January 1993

A:Note: in Genbank entry RMC3RA, release 113.0, the source is designated as Rattus r

C:Genetics:

A:Gene: MC3-R

C:Superfamily: melanocortin receptor

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 56.2%; Score 971; DB 2; Length 323;

Best Local Similarity 59.7%; Pred. No. 5.5e-72;

Matches 182; Conservative 53; Mismatches 62; Indels 8; Gaps 4;

QY 17 NRSTYGPHSNASBSLGKGYSDGCYEQLFVSPFVTLGVISLLENILVIAIAKNKLNH 76

16 NLSOHPAAPSASNRSGSGF---C-EQVFKPEVFLALGIVSLMENILVILAVVRGNLH 70

QY 77 SPMYFICSLAVADMVLSVNSGETIVILLNSTD-TDAQSFVTNDVNDWIDSVICSSLLA 135

71 SPMYFFLLSLQADMVLSNLSLNTIMVINSDSLTLDEQFTHQNDNFDSMICISLVA 130

QY 136 SICSLSLIAVDRTFTFYALQYHNIMTVRRVGIISCIWAACITVSGVLFTIYSDSSAVII 195

131 SICNLGLAIAVDRTVTFYALRHSIMTVRKALSLIVAIWCCGICGVMFIVSESXKIV 190

QY 196 CLITMFTMALMASLYVHMFMLARLHRIKRIAVLPQGTI--RQGANMGKAITLTILGV 253

191 CLITMFFAVLLMGTLVIMFLFARLHVQRIALPADGVAPOQHSCMKMGAVTITILGV 250

QY 254 FVVCWAPFFLHLIFYISCPQNPYCVCFMSGHFNLYLLIMCNSIIDPLIYALRSQELKTF 313

251 FIFCWAPFFLHLIITCPTNPYICYTAHFNTYLLVLMCNSVIDPLIYAFRSLRLNTF 310

314 KETIC 318

Db 311 KEILC 315

||||

RESULT 10
I46416
melanocyte-stimulating hormone receptor - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 24-Sep-1999
C:Accession: I46416; S43120
J:Barrett, P.; Macdonald, A.; Helliwell, R.; Davidson, G.; Morgan, P.
J. Mol. Endocrinol. 12, 203-213, 1994
A:Title: Cloning and expression of a new member of the melanocyte-stimulating hormone
A:Reference number: I46416; MUID:94338523; PMID:8060485
A:Accession: I46416
A>Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-325 <BAR>
A:Cross-references: EMBL:Z31369; NID:9467692; PIDN:CAA83239.1; PID:9467693
A:Note: submitted to the EMBL Data Library, March 1994
C:Superfamily: melanocortin receptor

Query Match 55.9%; Score 965.5; DB 2: Length 325;
Best Local Similarity 59.2%; Pred. No.1: 6e-71;

Matches 197; Conservative 42; Mismatches 85; Indels 9; Gaps 4;									
Qy	1	MNSTHRCMTSLHFWNRSTYGPHSNASLSGKGYSDGCVQOLFVSPFVTLGLVSL 60							
Db	1	MNSSFH-----LHFLDLGLNATGPNLS-GLSVRNASSPC-EDMGIAVEFLAUGLSLL 52							
Qy	61	ENILVTVIAKKNLHSPMTFFTCISLAVADMLVSVNSGSETIVITLL-NSTDTDQAQFTV 119							
Db	53	ENILVIGAIVRNRLHPMTFFVGLAVADMLVSLSNFETITITLLTNKHLVNADASVR 112							
Qy	120	NIDNVIDVSCSLASISLSTAVDRYETIFALQYHNTVMVRRVGIISCIWAQCTV 179							
Db	113	HLDNVFSMICISVWASMCSLAIVDRYVITFCRLYQRIMTGRRSGLIAGIWFCTS 172							
Qy	180	SGVLFIYSDSSAVIICLIIMFFMTLMALMASLYVHMFMLHRIKRIAVLPDGTITROGA 239							
Db	173	CGTVFIYVYESTYVVCVLIAMFLTMLLMASLTHMFLARTVRRITAAPLGHSSVQRT 232							
Qy	240	NMGAIPTLTLIGVVFVVCWAPFHLHFIYISCPQNPYCVCFMSHFNLYLILMCSNIIDP 299							
Db	233	GVKGATLMLGLVFIICWAPFHLHFIYISCPQNPYCVCFMSHFNLYLILMCSNIIDP 292							
Qy	300	LIYALRSQELRKTFKEIICYPGLGCLDSRY 332							
Db	293	LIYAFRSQEMRKTFKEIVCFQGRTPCRFPSTY 325							
RESULT 11									
S71420									
melanocortin 1 receptor - chicken									
C:Species: Gallus gallus (chicken)									
C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 04-Sep-1998									
R:Takeuchi, S.; Suzuki, H.; Yabuuchi, M.; Takahashi, S.									
Biochim. Biophys. Acta 1308, 164-168, 1996									
A:Title: A possible involvement of melanocortin 1-receptor in regulating feather color									
A:Reference number: S71420; MUID:96350469; PMID:8764834									
A:Accession: S71420									
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra									
A:Molecule type: DNA									
A:Residues: 1-314 <TAK>									
C:Superfamily: melanocortin receptor									
Query Match 48.2%; Score 832.5; DB 2; Length 314;									
Best Local Similarity 51.5%; Pred. No. 1.1e-60;									
Matches 157; Conservative 63; Mismatches 78; Indels 7; Gaps 3;									
Qy	16	WNRSTYGPHSNASLSGKGYSDGCVQOLFVSPFVTLGLVSLLENILVIAIAKNKL 75							
Db	14	WNASE-GNQSNATAGAGGACQ-----LDIPNELFTLGLVSLVENLLVAAILKRNKL 67							
Qy	76	HSPMYFFICSLAVADMLVSVNSGSETIVITLL-NSTDTDQAQFTVNDNVIDSVICSLL 134							
Db	68	HSPMYFFICCLAVSDMLVSVNSLAETFLMELMEHGVILVIRASIVRHMNDVIMLCSSV 127							
Qy	135	ASICSLLSIAVDRTIFAYALQYHNTVMVRRVGIISCIWAQCTVSGVLFIIYSDSSAVI 194							
Db	128	SSLFLGVIAVDRTIAFYALRHSIMTLQRAVVTMASVWLASTVSTVLTITYRNAIL 187							
Qy	195	ICLTIMFTMLMALMSLYVHMFMLARLHRIKRIAVLPDGTITROGANKMGATITLIGVF 254							
Db	188	LCLIGFLEMLVLMVLYIHMFLARHHRVRSISSQKQPTIYRTSSLKGVATLILGVF 247							
Qy	255	VWCWAPFHLHFIYISCPQNPYCVCFMSHFNLYLILMCSNIIDPLIYALRSQELRKTFK 314							
Db	248	FICWGPFFHLIIVTCTPNPFCCTFFSYFNFLILICNSVVDPLIYAFRSQELRRTL 307							
Qy	315	EIICC 319							
Db	308	EWLVC 312							
RESULT 13									
S45708									
MSH receptor - bovine									
C:Species: Bos primigenius taurus (cattle)									
C:Date: 10-Dec-1994 #sequence_revision 19-Apr-1996 #text_change 20-Apr-2000									
R:Accession: S45708									
R:Vanetti, M.; Schoenrock, C.; Meyerhof, W.; Hoellt, V.									
FEBS Lett. 346, 268-272, 1994									
A:Title: Molecular cloning of a bovine MSH receptor which is highly expressed in the									
A:Reference number: S45708; MUID:94307438; PMID:8034052									
A:Accession: S45708									
A:Status: preliminary									

S70005									
melanocortin 1 receptor - chicken									
C:Species: Gallus gallus (chicken)									
C:Date: 15-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000									
R:Takeuchi, S.; Suzuki, H.; Hirose, S.; Yabuuchi, M.; Sato, C.; Yamamoto, H.; Takahashi, S.									
Biochim. Biophys. Acta 1306, 122-126, 1996									
A:Title: Molecular cloning and sequence analysis of the chick melanocortin 1-receptor									
A:Reference number: S70005; MUID:96221280; PMID:8634326									
A:Accession: S70005									
A:Molecule type: DNA									
A:Residues: 1-314 <TAK>									
A:Cross-references: EMBL:D78272									
R:Takeuchi, S.									
submitted to the EMBL Data Library, November 1995									
A:Reference number: S72884									
A:Accession: S72884									
A:Molecule type: DNA									
A:Residues: 1-9,'V',11-217,'S',219-314 <TAW>									
A:Cross-references: EMBL:D78272; NID:q1065994; PIDN:BAAL1336.1; PID:g1065995									
C:Superfamily: melanocortin receptor									
C:Keywords: G protein-coupled receptor; glycoprotein; lipoprotein; thiolester bond; t									
F:36-61/Domain: transmembrane #status predicted <TM1>									
F:71-95/Domain: transmembrane #status predicted <TM2>									
F:114-138/Domain: transmembrane #status predicted <TM3>									
F:162-181/Domain: transmembrane #status predicted <TM4>									
F:193-209/Domain: transmembrane #status predicted <TM5>									
F:237-263/Domain: transmembrane #status predicted <TM6>									
F:276-297/Domain: transmembrane #status predicted <TM7>									
F:15,20,23/Binding site: carbohydrate (Asn) (covalent) #status predicted									
F:312/Binding site: palmitate (Cys) (covalent) #status predicted									
Query Match 47.4%; Score 819.5; DB 2; Length 314;									
Best Local Similarity 50.8%; Pred. No. 1.3e-59;									
Matches 155; Conservative 64; Mismatches 79; Indels 7; Gaps 3;									
Qy	16	WNRSTYGPHSNASLSGKGYSDGCVQOLFVSPFVTLGLVSLLENILVIAIAKNKL 75							
Db	14	WNASE-GNQSNATAGAGGACQ-----LDIPNELFTLGLVSLVENLLVAAILKRNKL 67							
Qy	76	HSPMYFFICSLAVADMLVSVNSGSETIVITLL-NSTDTDQAQFTVNDNVIDSVICSLL 134							
Db	68	HSPTYFFICCLAVSDMLVSVNSLAKTLFMLMEHGVILVIRASIVRHMNDVIMLCSSV 127							
Qy	135	ASICSLLSIAVDRTIFAYALQYHNTVMVRRVGIISCIWAQCTVSGVLFIIYSDSSAVI 194							
Db	128	SSLFLGVIAVDRTIAFYALRHSIMTLQRAVVTMASVWLASTVSTVLTITYRNAIL 187							
Qy	195	ICLTIMFTMLMALMSLYVHMFMLARLHRIKRIAVLPDGTITROGANKMGATITLIGVF 254							
Db	188	LCLIGFLEMLVLMVLYIHMFLARHHRVRSISSQKQPTIYRTSSLKGVATLILGVF 247							
Qy	255	VWCWAPFHLHFIYISCPQNPYCVCFMSHFNLYLILMCSNIIDPLIYALRSQELRKTFK 314							
Db	248	FICWGPFFHLIIVTCTPNPFCCTFFSYFNFLILICNSVVDPLIYAFRSQELRRTL 307							
Qy	315	EIICC 319							
Db	308	EWLVC 312							
RESULT 13									
S45708									
MSH receptor - bovine									
C:Species: Bos primigenius taurus (cattle)									
C:Date: 10-Dec-1994 #sequence_revision 19-Apr-1996 #text_change 20-Apr-2000									
R:Accession: S45708									
R:Vanetti, M.; Schoenrock, C.; Meyerhof, W.; Hoellt, V.									
FEBS Lett. 346, 268-272, 1994									
A:Title: Molecular cloning of a bovine MSH receptor which is highly expressed in the									
A:Reference number: S45708; MUID:94307438; PMID:8034052									
A:Accession: S45708									
A:Status: preliminary									

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OM protein - protein search, using sw model

Run on: June 4, 2003, 18:04:01 ; Search time 14 seconds
(without alignments)
983.581 Million cell updates/sec

Title: US-09-884-211a-3

Perfect score: 1728

Sequence: 1 MNSTHHGHMTSLHFNWRS.....FKELICCYPLGGCLDLSSRY 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1698	98.3	332	1	MC4R_PIG
2	1659.5	96.0	332	1	MC4R_HUMAN
3	1652	95.6	332	1	MC4R_RAT
4	1604	92.8	332	1	MC4R_BOVIN
5	1047	60.6	325	1	MC5R_RAT
6	1030.5	59.6	325	1	MC5R_PANTR
7	1030	59.6	325	1	MC5R_MOUSE
8	1026.5	59.4	325	1	MC5R_HUMAN
9	1000.5	57.9	323	1	MC3R_MOUSE
10	988.5	57.2	360	1	MC3R_HUMAN
11	972.5	56.3	325	1	MC5R_BOVIN
12	971	56.2	323	1	MC3R_RAT
13	965.5	55.9	325	1	MC5R_SHEEP
14	939	54.3	294	1	MC5R_PIG
15	932	53.9	184	1	MC4R_MOUSE
16	819.5	47.4	314	1	MSHR_CHICK
17	777.5	45.0	317	1	MSHR_CAPCA
18	777.5	45.0	317	1	MSHR_DANDA
19	775.5	44.9	317	1	MSHR_BOVIN
20	773.5	44.8	317	1	MSHR_ALCAA
21	767.5	44.4	317	1	MSHR_CAPHI
22	767.5	44.4	317	1	MSHR_SHEEP
23	765.5	44.3	317	1	MSHR_CEREL
24	765.5	44.3	317	1	MSHR_OVIMO
25	765	44.3	317	1	MSHR_RANTA
26	763	44.2	317	1	MSHR_CANFA
27	763	44.2	317	1	MSHR_VULVU
28	760.5	44.0	283	1	MSHR_PIG
29	754.5	43.7	315	1	MSHR_MOUSE
30	754.5	43.7	317	1	MSHR_HUMAN
31	750.5	43.4	317	1	MSHR_PANTR
32	733.5	42.4	292	1	MSHR_HORSE
33	721	41.7	297	1	ACTR_HUMAN

34 718 41.6 295 1 ACTR_SHEEP
35 717 41.5 297 1 ACTR_BOVIN
36 711 41.1 296 1 ACTR_MOUSE
37 709 41.0 297 1 ACTR_MESAU
38 684 39.6 297 1 ACTR_CAVPO
39 361 20.9 364 1 EDG2_MOUSE
40 356.5 20.6 364 1 EDG2_HUMAN
41 354 20.5 393 1 EDG2_SHEEP
42 351 20.3 364 1 EDG2_BOVIN
43 341.5 19.8 334 1 GP12_HUMAN
44 331.5 19.2 334 1 GP12_RAT
45 328.5 19.0 383 1 EDG1_RAT

ALIGNMENTS

RESULT 1

MC4R_PIG

ID MC4R_PIG STANDARD; PRT; 332 AA.
AC O97504: Q9N274; Q9N141;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melanocortin-4 receptor (MC4-R).
GN MC4R.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-LND; TISSUE-Kidney;
RA Ito Y., Minezawa M.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 73-320 FROM N.A., AND VARIANT ASN-298.
RX MEDLINE=20122164; PubMed=10656927;
RA Kim K.S., Larsen N., Short T., Plastow G., Rothschild M.F.;
RT "A missense variant of the porcine melanocortin-4 receptor (MC4R) gene
is associated with fatness, growth, and feed intake traits.";
Mamm. Genome 11:131-135(2000).
RN [3]
RP SEQUENCE OF 75-142 FROM N.A.
RC TISSUE-Hypothalamus;
RA Matteri R.L., Dyer C.J.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECEPTOR SPECIFIC TO THE HEPTAPEPTIDE CORE COMMON TO
ADRENOCORTICOTROPIC HORMONE AND ALPHA-, BETA-, AND GAMMA-MSH.
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE
CYCLASE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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EMBL; AB021664; BAA36170.1; -
EMBL; AF087937; AAF31753.1; -
EMBL; AF227727; AAF34778.1; -
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHDOPSN
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_FL1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEPTOR_FL2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
Phosphorylation; Lipoprotein; Palmitate; Polymorphism.
FT DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).

FT	TRANSNEM	44	69	1 (POTENTIAL).	
FT	DOMAIN	70	81	CYTOPLASMIC (POTENTIAL).	
FT	TRANSNEM	82	106	2 (POTENTIAL).	
FT	DOMAIN	107	123	EXTRACELLULAR (POTENTIAL).	
FT	TRANSNEM	124	145	3 (POTENTIAL).	
FT	DOMAIN	146	165	CYTOPLASMIC (POTENTIAL).	
FT	TRANSNEM	166	186	4 (POTENTIAL).	
FT	DOMAIN	187	191	EXTRACELLULAR (POTENTIAL).	
FT	TRANSNEM	192	215	5 (POTENTIAL).	
FT	DOMAIN	216	248	CYTOPLASMIC (POTENTIAL).	
FT	TRANSNEM	249	271	6 (POTENTIAL).	
FT	DOMAIN	272	280	EXTRACELLULAR (POTENTIAL).	
FT	TRANSNEM	281	304	7 (POTENTIAL).	
FT	DOMAIN	305	332	CYTOPLASMIC (POTENTIAL).	
FT	CARBOHYD	2	2	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	17	17	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	26	26	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	LIPID	318	318	PALMITATE (POTENTIAL).	
FT	VARIANT	298	298	D -> N (ASSOCIATED WITH LESS BACKFAT	
FT				THICKNESS, SLOWER GROWTH RATE AND LOWER	
FT				FEED INTAKE).	
SO	SEQUENCE	332 AA; 36946 MW; 5CD1CD67008BFC81	CRC64;		
Query Match					98.3%; Score 1698; DB 1; Length 332;
Best Local Similarity					98.2%; Pred. No. 3.8e-105;
Matches 326; Conservative					3; Mismatches 3; Indels 0; Gaps 0;
QY	1	MNSTHHGHTSLHFWNRSTYGHPSNASESLKAGYSDGGCYQLFVSPFVTLGVISLL	60		
Db	1	MNSTHHGHTSLHFWNRSTYGLHNSASEPLKGYSEGCGYQLFVSPFVTLGVISLL	60		
QY	61	ENILVTAIAKNNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN	120		
Db	61	ENILVTAIAKNNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN	120		
QY	121	INVIDSVICSSLLASICSLSTAVDRYETIYALQYHNMVRRVGVIIISCIWAACVTS	180		
Db	121	INVIDSVICSSLLASICSLSTAVDRYETIYALQYHNMVRRVGVIIISCIWAACVTS	180		
QY	181	GVLFIIYDSSAVIICLIITMFTMLMALASLVHMFIMARLHKRIAVLPSTGTIRQGAN	240		
Db	181	GVLFIIYDSSAVIICLIITVFTMLMALASLVHMFIMARLHKRIAVLPSTGTIRQGAN	240		
QY	241	MKGATLTLLIGVVCWAPFELHLIFITSCPNPYCVCFMSHENLYLILMCNLSIIDPL	300		
Db	241	MKGATLTLLIGVVCWAPFELHLIFITSCPNPYCVCFMSHENLYLILMCNLSIIDPL	300		
QY	301	IYALRSQELRKTFFKEIICCYPLGGCLDSRY	332		
Db	301	IYALRSQELRKTFFKEIICCYPLGGCLDSRY	332		
RESULT 2					
MC4R_HUMAN STANDARD; PRT: 332 AA.					
ID	MC4R_HUMAN				
AC	F32245; Q16317;				
DT	01-OCT-1993 (Rel. 27, Created)				
DT	01-OCT-1993 (Rel. 27, Last sequence update)				
DE	16-OCT-2001 (Rel. 40, Last annotation update)				
GN	Melanocortin-4 receptor (MC4-R).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=93315499; PubMed=8392067;				
RA	Gantz I., Miwa H., Konda Y., Shimoto Y., Tashiro T., Waston S.J.,				
RA	Delvalle J.;				
RT	"Molecular cloning, expression, and gene localization of a fourth				
RT	melanocortin receptor.";				
RL	J. Biol. Chem. 268:15174-15179(1993).				

RN	1 (POTENTIAL).				
RP	CYTOPLASMIC (POTENTIAL).				
RX	MEDLINE=95157557; PubMed=7854347;				
RA	Mountjoy K.G., Mortrud M.T., Low M.J., Simerly R.B., Cone R.D.;				
RT	"Localization of the melanocortin-4 receptor (MC4-R) in				
RT	neuroendocrine and autonomic control circuits in the brain.";				
RL	Mol. Endocrinol. 8:1298-1308(1994).				
RN	3 (POTENTIAL).				
RP	EXTRACELLULAR (POTENTIAL).				
RX	MEDLINE=99213892; PubMed=10199800;				
RA	Hinney A., Schmidt A., Nottelboom K., Heibult O., Becker I., Ziegler A.,				
RA	Gerber G., Sina M., Gorg T., Mayer H., Siegfried W., Fichter M.,				
RA	Remschmidt H., Hebebrand J.;				
RT	"Several mutations in the melanocortin-4 receptor gene including a				
RT	nonsense and a frameshift mutation associated with dominantly				
RL	inherited obesity in humans.";				
RL	J. Clin. Endocrinol. Metab. 84:1483-1486(1999).				
CC	-1- FUNCTION: RECEPTOR SPECIFIC TO THE HEPTAPEPTIDE CORE COMMON TO				
CC	ADRENOCORTICOTROPIC HORMONE AND ALPHA-, BETA-, AND GAMMA-MSH.				
CC	THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE				
CC	CYCLASE.				
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	-1- TISSUE SPECIFICITY: BRAIN, PLACENTAL, AND GUT TISSUES.				
CC	-1- DISEASE: DEFECTS IN MC4R SEEM TO PLAY A ROLE IN THE GENETIC				
CC	PREDISPOSITION TO OBESITY.				
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; L08603; AAA35791.1; -;				
DR	EMBL; S77415; AAB33341.1; -;				
DR	PIR; A47111; A47111.				
DR	Genew; HGNC:6932; MC4R.				
DR	MIM; 155541; -;				
DR	InterPro; IPR000276; GPCR_Rhodpsn.				
DR	Pfam; PF00001; 7tm1.1.				
DR	PROSITE; PS00337; G-PROTEIN_RECEP_FL_1; 1.				
DR	PROSITE; PS00362; G-PROTEIN_RECEP_FL_2; 1.				
KW	Phosphorylation; Lipoprotein; Transmembrane; Glycoprotein;				
KW	Disease mutation; Obesity.				
FT	DOMAIN 1 43				EXTRACELLULAR (POTENTIAL).
FT	TRANSNEM 44 69				1 (POTENTIAL).
FT	DOMAIN 70 81				CYTOPLASMIC (POTENTIAL).
FT	TRANSNEM 82 106				2 (POTENTIAL).
FT	DOMAIN 107 123				EXTRACELLULAR (POTENTIAL).
FT	TRANSNEM 124 145				3 (POTENTIAL).
FT	DOMAIN 146 165				CYTOPLASMIC (POTENTIAL).
FT	TRANSNEM 166 186				4 (POTENTIAL).
FT	DOMAIN 187 191				EXTRACELLULAR (POTENTIAL).
FT	TRANSNEM 192 215				5 (POTENTIAL).
FT	DOMAIN 216 248				CYTOPLASMIC (POTENTIAL).
FT	TRANSNEM 249 271				6 (POTENTIAL).
FT	DOMAIN 272 280				EXTRACELLULAR (POTENTIAL).
FT	TRANSNEM 281 304				7 (POTENTIAL).
FT	DOMAIN 305 332				CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD 3 3				N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 17 17				N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 26 26				N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	LIPID 318 318				PALMITATE (POTENTIAL).
FT	VARIANT 30 30				S -> R (IN OBESITY).
FT					/FTID=VAR_010704.
FT	VARIANT 37 37				D -> V (IN OBESITY).
FT					/FTID=VAR_010705.
FT	VARIANT 78 78				P -> L (IN OBESITY).
FT					/FTID=VAR_010706.
FT	VARIANT 103 103				I -> V.


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FT VARIANT 112 112 /FTid=VAR_010707.
FT T -> M (IN OBESITY).
FT FTid=VAR_010708.
FT VARIANT 165 165 R -> W (IN OBESITY).
FT FTid=VAR_010709.
FT VARIANT 251 251 I -> L.
FT FTid=VAR_010710.
FT VARIANT 252 252 G -> S (IN OBESITY).
FT FTid=VAR_010711.
FT VARIANT 317 317 I -> T (IN OBESITY).
FT FTid=VAR_010712.
FT CONFLICT 169 169 I -> S (IN REF. 2).
FT SEQUENCE 332 AA; 36956 MW; 1C89752CF4DF30C CRC64;

Query Match 96.08; Score 1659.5; DB 1; Length 332;
Best Local Similarity 96.78; Pred. No. 1.3e-102;
Matches 321; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

Qy 1 MNSTHHGHTSLHFWNRSTYGPNSNASESLGKGYSDGCGYQLFVSPVFTLGVISLL 60
Db :||| | ||||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
2 VNST-HRGMTSLHLNRRSHLHNSNASESLGKGYSDGCGYQLFVSPVFTLGVISLL 60

Qy 61 ENILVIVIAKNNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
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Qy 121 IDNVDSVICSLLASCSLLSIADVRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
Db :||| | ||||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 IDNVDSVICSLLASCSLLSIADVRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180

Qy 121 IDNVDSVICSLLASCSLLSIADVRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
Db :||| | ||||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 IDNVDSVICSLLASCSLLSIADVRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180

Qy 181 GVLFIYSDSSAVIICLITMFTMLMALMSLYVHMFMLARLHKRIAVLPCTGTIROGAN 240
Db :||| | ||||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 GILFIYSDSSAVIICLITMFTMLMALMSLYVHMFMLARLHKRIAVLPCTGTIROGAN 240

Qy 241 MKGAITITLIGVFWVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMCSNIDPL 300
Db :||| | ||||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
241 MKGAITITLIGVFWVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMCSNIDPL 300

Qy 301 IYALRSQELRKTKEIICCPYGLGCLDSRY 332
Db :||| | ||||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 IYALRSQELRKTKEIICCPYGLGCLDSRY 332
```

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RESULT 3
MC4R_RAT
ID MC4R_RAT STANDARD; PRT; 332 AA.
AC P70596;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Melanocortin-4 receptor (MC4-R).
GN MC4R.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=96387362; PubMed=8794897;
RA Alvaro J.D., Tatiro J.B., Quillan J.M., Fogliano M., Eisenhard M.,
RA Lerner M.R., Nestler E.J., Duman R.S.;
RT "Morphine down-regulates melanocortin-4 receptor expression in brain
RT regions that mediate opiate addiction."
RL Mol. Pharmacol. 50:583-591(1996).
RC -1- FUNCTION: RECEPTOR SPECIFIC TO THE HEPTAPEPTIDE CORE COMMON TO
CC ADRENOCORTICOTROPIC HORMONE AND ALPHA-, BETA-, AND GAMMA-MSH.
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE
CC CYCLASE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: BRAIN, ENRICHED IN THE STRIATUM, NUCLEUS
CC ACCUMBENS, AND PERIAQUE-DUCTAL GRAY.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U67863; AAB36517.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECF1_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECF1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 44 69 1 (POTENTIAL).
FT DOMAIN 70 81 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 82 106 2 (POTENTIAL).
FT DOMAIN 107 123 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 124 145 3 (POTENTIAL).
FT DOMAIN 146 165 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 166 186 4 (POTENTIAL).
FT DOMAIN 187 191 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 192 215 5 (POTENTIAL).
FT DOMAIN 216 248 6 (POTENTIAL).
FT TRANSMEM 249 271 7 (POTENTIAL).
FT DOMAIN 272 280 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 281 304 7 (POTENTIAL).
FT DOMAIN 305 332 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 2 2 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 17 17 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 26 26 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 318 318 PALMITATE (POTENTIAL).
SQ SEQUENCE 332 AA; 36986 MW; E0E9BAC7E7D168E6 CRC64;

Query Match 95.6%; Score 1652; DB 1; Length 332;
Best Local Similarity 95.2%; Pred. No. 4.1e-102;
Matches 316; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MNSTHHGHTSLHFWNRSTYGPNSNASESLGKGYSDGCGYQLFVSPVFTLGVISLL 60
Db :||| | ||||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 MNSTHHGHTSLHFWNRSHLHNSNASESLGKGYSDGCGYQLFVSPVFTLGVISLL 60

Qy 61 ENILVIVIAKNNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
Db :||| | ||||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 ENILVIVIAKNNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120

Qy 121 IDNVDSVICSLLASCSLLSIADVRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
Db :||| | ||||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 IDNVDSVICSLLASCSLLSIADVRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180

Qy 181 GVLFIYSDSSAVIICLITMFTMLMALMSLYVHMFMLARLHKRIAVLPCTGTIROGAN 240
Db :||| | ||||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 GVLFIYSDSSAVIICLITMFTMLMALMSLYVHMFMLARLHKRIAVLPCTGTIROGAN 240

Qy 241 MKGAITITLIGVFWVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMCSNIDPL 300
Db :||| | ||||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
241 MKGAITITLIGVFWVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMCSNIDPL 300

Qy 301 IYALRSQELRKTKEIICCPYGLGCLDSRY 332
Db :||| | ||||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 IYALRSQELRKTKEIICCPYGLGCLDSRY 332

RESULT 4
MC4R_BOVIN
ID MC4R_BOVIN STANDARD; PRT; 332 AA.
AC Q9GLJ8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
```

DE Melanocortin-4 receptor (MC4-R).
 GN MC4R.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANTS ALA-145 AND THR-172.
 RC STRAIN-Holstein;
 RA Haegeman A., Coopman F., Jacobs K., Mattheeuws M., Van Zeveren A.,
 RA Peelman L.J.;
 RT "Bovine melanocortin receptor 4: cDNA sequence, polymorphisms and
 mapping.";
 RL Anim. Genet. 32:189-192(2001).
 CC -1- FUNCTION: RECEPTOR SPECIFIC TO THE HEPTAPEPTIDE CORE COMMON TO
 CC ADRENOCORTICOTROPIC HORMONE AND ALPHA-, BETA-, AND GAMMA-MSH.
 CC THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE
 CC CYCLASE (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF265221; AAG17639.1; -
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G-PROTEIN_RECEPTOR_F1_1; 1.
 DR PROSITE; PS00262; G-PROTEIN_RECEPTOR_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Phosphorylation; Lipoprotein; Palmitate; Polymorphism.
 FT DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 44 69 1 (POTENTIAL).
 FT DOMAIN 70 81 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 82 106 2 (POTENTIAL).
 FT DOMAIN 107 123 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 124 145 3 (POTENTIAL).
 FT DOMAIN 146 165 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 166 186 4 (POTENTIAL).
 FT DOMAIN 187 191 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 192 215 5 (POTENTIAL).
 FT DOMAIN 216 248 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 249 271 6 (POTENTIAL).
 FT DOMAIN 272 280 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 281 304 7 (POTENTIAL).
 FT DOMAIN 305 332 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 2 2 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 17 17 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 26 26 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT LIPID 318 318 PALMITATE (POTENTIAL).
 FT VARIANT 145 145 V -> A.
 FT VARIANT 172 172 A -> T.
 SQ SEQUENCE 332 AA; 36620 MW; C28356955F9D8FBD CRC64;
 Query Match 92.8%; Score 1604; DB 1; Length 332;
 Best Local Similarity 94.3%; Pred. No. 5.8e-99;
 Matches 313; Conservative 6; Mismatches 13; Indels 0; Gaps 0;
 QY 1 MNSTHHGHGHTSLHFWNRSTYGFPHSNVASESLGKYSDDGCGYQLFVSPFVFTLGVISLL 60
 Db 1 MNSTPLGHTSLHWSNRSAHGMPTNVSESLAGKYSDDGCGYQLFVSPFVFTLGVISLL 60
 QY 61 ENILVIVALKNNLHSPMYFFICSLAVADMVLSVNSGSETIVITLLNSTDIDAQSFVN 120
 Db 61 ENILVIVALKNNLHSPMYFFICSLAVADMVLSVNSGSETIVITLLNSTDIDAQSFVD 120

QY 121 IDNVDSVICSSLLASICSLLSIADVRYFTFYALQVHNIMTVRRVGIISCIWAACVTS 180
 Db 121 IDNVDSVICSSLLASICSLLSIADVRYFTFYALQVHNIMTVRRVGIISCIWAACVTS 180
 QY 181 GVLFIYSDSSAVIICLIITNFFMTLMALMASLYVHMFELMARLHKRIAVLPGTGTIROGAN 240
 Db 181 GVLFIYSDSSAVIICLIITNFFMTLMALMASLYVHMFELMARLHKRIAVLPGTGTIROGAN 240
 QY 241 MKGAITLTILIGVVFVVCWAPFFLHLIFYISCPNPYCVCFMSHFNLYLILIMCNSIIDPL 300
 Db 241 MKGAITLTILIGVVFVVCWAPFFLHLIFYISCPNPYCVCFMSHFNLYLILIMCNSIIDPL 300
 QY 301 IYALRSQELRKTEKEIICCYPLGLGLCDLSRY 332
 Db 301 IYALRSQELRKTEKEIICCYPLGLGLCDLSRY 332
 RESULT 5
 MCSR_RAT
 ID MCSR_RAT STANDARD; PRT; 325 AA.
 AC P35345;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Melanocortin-5 receptor (MC5-R).
 GN MC5R.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=101116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Striatum.
 RX MEDLINE=94234987; PubMed=8179577;
 RA Griffon N., Mignon V., Facchinetti P., Diaz J., Schwartz J.C.,
 RA Sokoloff P.;
 RT "Molecular cloning and characterization of the rat fifth melanocortin
 RT receptor.";
 RL Biochem. Biophys. Res. Commun. 200:1007-1014(1994).
 CC -1- FUNCTION: RECEPTOR FOR MSH (ALPHA, BETA AND GAMMA) AND ACTH. THE
 CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
 CC ADENYLATE CYCLASE. THIS RECEPTOR IS A POSSIBLE MEDIATOR OF THE
 CC IMMUNOMODULATION PROPERTIES OF MELANOCORTINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: VERY LOW EXPRESSION LEVELS IS DETECTED IN
 CC BRAIN, WHILE HIGH LEVELS ARE FOUND IN ADRENALS, STOMACH, LUNG AND
 CC SPLEEN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL; L27081; AAA41577.1; -
 DR PIR; JC2193; JC2193. GPCR_Rhodpsn.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PROSITE; PS00237; G-PROTEIN_RECEPTOR_F1_1; 1.
 DR PROSITE; PS00262; G-PROTEIN_RECEPTOR_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 37 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 38 61 1 (POTENTIAL).
 FT DOMAIN 62 73 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 74 97 2 (POTENTIAL).
 FT DOMAIN 98 114 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 115 138 3 (POTENTIAL).
 FT DOMAIN 139 155 CYTOPLASMIC (POTENTIAL).

```
FT TRANSMEM 156 179 4 (POTENTIAL).
FT DOMAIN 180 186 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 187 211 5 (POTENTIAL).
FT DOMAIN 210 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 242 265 6 (POTENTIAL).
FT DOMAIN 266 273 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 274 297 7 (POTENTIAL).
FT DOMAIN 298 325 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 2 2 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 15 15 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 28 28 N-LINKED (GLCNAC. .) (POTENTIAL).
FT LIPID 311 311 PALMITATE (POTENTIAL).
FT LIPID 312 312 PALMITATE (POTENTIAL).
SQ SEQUENCE 325 AA; 37050 MW; 4E19FF1ABE9A6BDC CRC64;

Query Match 60.6%; Score 1047; DB 1; Length 325;
Best Local Similarity 65.0%; Pred. No. 2.4e-62;
Matches 202; Conservative 46; Mismatches 59; Indels 4; Gaps 3;

Qy 26 NASES--LGKGYSD-GGCEYQLFVSPVFTGLVGLISLENILVIVAIKNNLHSPMYFF 82
Db 15 NASEDNLGQNVNKKSSACEDMGIAVEFLTGLVGLISLENILVIGAIKNNLHSPMYFF 74

Qy 83 ICSLAVADMLVSVNGSETIVITLLNSTD-TDAQSFVNIDNVDVSCSLASICSLL 141
Db 75 VGSILAVADMLVSMNAWETITVILNNKHVVIAIDFVHRHDNVFDSMICSIVASMCSSL 134

Qy 142 SIADVRYFTFYALQYHNIMTVRVGIIICSIWAACTVSGVLFIIYSDSSAVIICLTMP 201
Db 135 AIADVRYFTFYALRYHHIMTVARRSGVIIACIWFICSGVFIYIYVESYVIVCLISMF 194

Qy 202 FTMLALMASLYVHFMFLMARLHKRIKRIAVLPGTGTROGANKMGATLTILIGVFVVCWAPF 261
Db 195 FTMLFFVSVLYIHFLLARHVRKRIASPRYSVQRASMGATLTILWLGIFVVCWSPF 254

Qy 262 FLHLIFVISCQPNVYCVCFMSHFNLXLLILMCSNIDPLIYALRSQBLRKFKEIICYP 321
Db 255 FLHLILMISCQPNVYCVCFMSHFNLXLLILMCSNIDPLIYALRSQBLRKFKEIICCHG 314

Qy 322 LGLGLDLSRRY 332
Db 315 FRRTCTLLGRY 325

RESULT 6
MC5R_PANTR
ID MC5R_PANTR STANDARD; PRY; 325 AA.
AC Q9RT23;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Melanocortin-5 receptor (MC5-R).
GN MC5R.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21184529; PubMed=11286624;
RA Hattar N., Dixon C., Ray A.J., Phillips S.R., Cunliffe W.J., Dale M.,
RA Todd C., Meggit S., Birch-Machin M.A., Rees J.L.;
RT "Expression, candidate gene, and population studies of the
RT melanocortin 5 receptor."
RL J. Invest. Dermatol. 116:564-570(2001).
CC -!- FUNCTION: RECEPTOR FOR MSH (ALPHA, BETA AND GAMMA) AND ACTH. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
CC ADENYLATE CYCLASE. THIS RECEPTOR IS A POSSIBLE MEDIATOR OF THE
CC IMMUNOMODULATION PROPERTIES OF MELANOCORTINS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF208691; AAF19441.1;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 37 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 38 61 1 (POTENTIAL).
FT DOMAIN 62 73 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 74 97 2 (POTENTIAL).
FT DOMAIN 98 114 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 115 138 3 (POTENTIAL).
FT DOMAIN 139 155 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 156 179 4 (POTENTIAL).
FT DOMAIN 180 186 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 187 211 5 (POTENTIAL).
FT DOMAIN 212 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 265 6 (POTENTIAL).
FT DOMAIN 266 273 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 274 297 7 (POTENTIAL).
FT DOMAIN 298 325 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 2 2 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 15 15 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 20 20 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 28 28 N-LINKED (GLCNAC. .) (POTENTIAL).
FT LIPID 311 311 PALMITATE (POTENTIAL).
FT LIPID 312 312 PALMITATE (POTENTIAL).
SQ SEQUENCE 325 AA; 36646 MW; 9AFD17F0ACA059B8 CRC64;

Query Match 59.6%; Score 1030.5; DB 1; Length 325;
Best Local Similarity 62.0%; Pred. No. 2.9e-61;
Matches 206; Conservative 44; Mismatches 73; Indels 9; Gaps 4;

Qy 1 MNSTHRRHGMHTSLHFWNRSTYGPNSASESLGKGYSDGGCYEQLFVSPVFTGLVGL 60
Db 1 MNSSEH-----LHFLDLNLNATEGLSGPNVKNKS-SPC-EDMGIAVEVELTGLVGL 52

Qy 61 ENILVIVAIKNNLHSPMYFFICSLAVADMLVSVNGSETIVITLLNSTD-TDAQSFV 119
Db 53 ENILVIGAIKNNLHSPMYFFVCGSLAVADMLVSMSSAWETITVILLNKKHLVIADAFVR 112

Qy 120 NIDNVDSVICSLLASTICSLSTAVDRYFTFYALQYHNIMTVRVVGGIISCIWAACTV 179
Db 113 HIDNVDSMICSIVVASMCSLLAIVDRYFTFYALRYHHIMTVARRSGIITAGIWAFCG 172

Qy 180 SGVLIYSDSSAVIICLTITMFFTMLALMASLYVHFMFLMARLHKRIKRIAVLPCTGT 239
Db 173 CGIVFIYSESTVYILCLISMFAMFLVLSYIHFLLARHVRKRIALPRASSARQRT 232

Qy 240 NMKGATLTILIGVFVVCWAPFHLHIFVISCQPNVYCVCFMSHFNLXLLILMCSNIDP 299
Db 233 SMOGAVTVMLLGVFTVCWAPFHLHILMLSCPQLYSCFMSHFNLXLLILMCSNIDP 292

Qy 300 LIYALRSQBLRKFKEIICYPGLGLDLSRR 331
Db 293 LIYAFRSQBLRKFKEIICRCGFRACSFPRR 324

RESULT 7
MC5R_MOUSE
ID MC5R_MOUSE STANDARD; PRY; 325 AA.
AC P41149;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
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113 FLCSLAVADMVSVSNALETTIAIVHSIDYLTFFEDQFQHMNDNFDSMICSLVASICNL 172
141 LSHAVDRYFTFYALOVHNMVRRVGGIIISCIWAACVSGVLFIIYSDSAVICILITM 200
173 LAIAVDRTVTFYALRHSIMTVKATLVAIWWCCGCVGVFIVYSESKMWIVCLITM 232
201 FFTMLMASLYVHMFELMARLHKRIAPVPGTGI--ROGANMKGAITLTILIGVFFVVCW 258
233 FFAMLLMGTLVHMFELFARLHVKRIAPADGVAPOHSCMKGAVTITLLGVFFCW 292
259 APFELHLFIYSCPONPCVCFMSHFNLYLLIMCNSIIDPLIYALRSQELRKTFKEIC 318
293 APFELHLVLIITCTNPICYTAHENTYLVLMCNSVIDPLIYAFRSLELRNTFRELTC 352

RESULT 11
MC5R_BOVIN
ID MC3R_BOVIN STANDARD; PRT; 325 AA.
AC P56451;
DT 15-JUL-1998 (Rel. 36, Created)
DI 15-JUL-1998 (Rel. 36, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE Melanocortin-5 receptor (MC5-R).
GN MC3R.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Oulmouden A., Petit J.M., Julien R.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECEPTOR FOR MSH (ALPHA, BETA AND GAMMA) AND ACTH. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
CC ADENYLATE CYCLASE. THIS RECEPTOR IS A POSSIBLE MEDIATOR OF THE
CC IMMUNOMODULATION PROPERTIES OF MELANOCORTINS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; AJ002024; CAA05147.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1.1.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Phosphorylation; Lipoprotein; Palmitate.
CC DOMAIN 1 37 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 38 61 1 (POTENTIAL).
CC DOMAIN 62 73 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 74 97 2 (POTENTIAL).
CC DOMAIN 98 114 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 115 138 3 (POTENTIAL).
CC DOMAIN 139 155 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 156 179 4 (POTENTIAL).
CC DOMAIN 180 186 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 187 211 5 (POTENTIAL).
CC DOMAIN 212 239 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 240 265 6 (POTENTIAL).
CC DOMAIN 266 273 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 274 297 7 (POTENTIAL).
CC DOMAIN 298 325 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 326 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 2 2
CC CARBOHYD 15 15
```

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FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 311 311 PALMITATE (POTENTIAL).
SQ SEQUENCE 325 AA; 36525 MW; 81B6ACB2F12A09C7 CRC64;

Query Match 56.3%; Score 972.5; DB 1; Length 325;
Best Local Similarity 58.3%; Pred. No. 1.9e-57;
Matches 201; Conservative 39; Mismatches 72; Indels 33; Gaps 5;

QY 1 MNSHTHHGMHTSLHFWRNSTYCPHSNASESLGKGYSDGG-----CYEOLFVSP 48
   |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: |
Db 1 MNSSFH-----LHFLD-----LGLNTDGNLSGLSVQNASSLC-EDMGIAV 40
   |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: |
QY 49 EVFVTYGLISLENIIVIAIAKKNLHSPWFFICSLAVADMLVSVNGSGSTIVITLL- 107
   |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: |
Db 41 EVFLALGLISLENIIVIGAIVRNENLHTPMYFFVGLAVADMLVSLNSWETIYLLT 100
   |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: |
QY 108 NSTDTAQSFVTNIDNVDSVCSLASICSLASIAVDYRTFTFYALQYINIMTVRRVG 167
   |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: |
Db 101 NKHLVMADASVRHLNDNVPDSMICISVVASMCSLLAIAVDYRTFTFYALRYQRIMTGRSG 160
   |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: |
QY 168 IISCIWAACVSGVLFIIYSDSSNAVIICLITMTFMLALMASLYVHMFELMARLHKRTA 227
   |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: |
Db 161 AIIIGIWAFCASCCTVFIVYESTYVVICLAMEFLTMLLMASLYTHMFLARHRIA 220
   |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: |
QY 228 VLPGTGTIROGANMKGAITLTILIGVFFVVCWAPFLHLFIYSCPONPCVCFMSHFNLY 287
   |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: |
Db 221 TLPGHSSVRQRTGVKGAITLAMLGQFVFCWAPFLHLILMISCPHNLVYCSGFMSHFNY 280
   |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: |
QY 288 LILIMCNSIIDPLIYALRSQELRKTFKEICCYPLGGLCDLSRRY 332
   |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: |
Db 281 LILIMCNSVIDPLIYAFRSQEMRKTFKEICVFQSFRTPCRPPSY 325
   |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: |

RESULT 12
MC3R_RAT
ID MC3R_RAT STANDARD; PRT; 323 AA.
AC P32244;
DT 01-OCT-1993 (Rel. 27, Created)
DI 01-OCT-1993 (Rel. 27, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE Melanocortin-3 receptor (MC3-R).
GN MC3R.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Fischer; TISSUE=Hypothalamus;
RX MEDLINE=94022273; PubMed=8415620;
RA Roselli-Rehfuess L., Mountjoy K.G., Robbins L.S., Mortrud M.T.,
RA Low M.J., Simerly R.B., Cone R.D.;
RT "Identification of a receptor for gamma melanotropin and other
RT proopiomelanocortin peptides in the hypothalamus and limbic system.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:8856-8860(1993).
CC -1- FUNCTION: RECEPTOR FOR MSH (ALPHA, BETA AND GAMMA) AND ACTH.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: BRAIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; X70667; CAA50005.1; -
CC PIR; S36636; S36636.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1.1.
```



```
Db 293 LIYAFRQEMRKTFKEIVCFQGFRTPCRFSTY 325
|||||
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Melanocortin-5 receptor (Fragment).
MC5R.
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus...
NCBI_TaxID=9823;
[1]
SEQUENCE FROM N.A.
MEDLINE=20353873; PubMed=10895318;
Kim K.S., Marklund S., Rothschild M.F.;
"The proline melanocortin-5 receptor (MC5R) gene: polymorphisms,
linkage and physical mapping.";
Anim. Genet. 31:230-231(2000).
-1- FUNCTION: RECEPTOR FOR MSH (ALPHA, BETA AND GAMMA) AND ACTH. THE
ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
ADENYLATE CYCLASE. THIS RECEPTOR IS A POSSIBLE MEDIATOR OF THE
IMMUNOMODULATION PROPERTIES OF MELANOCORTINS.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-----
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
EMBL; AF133793; AAF82610.1; .
InterPro: IPR000276; GPCR_Rhodpsn.
Pfam: PF00001; 7tm_1; 1.
PRINTS: PF00237; GPCR_Rhodopsin.
PROSITE: PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
PROSITE: PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
NON_TER 1 1
DOMAIN <1 29 EXTRACELLULAR (POTENTIAL).
TRANSMEM 30 53 1 (POTENTIAL).
DOMAIN 54 65 CYTOPLASMIC (POTENTIAL).
TRANSMEM 66 89 2 (POTENTIAL).
DOMAIN 90 106 EXTRACELLULAR (POTENTIAL).
TRANSMEM 107 130 3 (POTENTIAL).
DOMAIN 131 147 CYTOPLASMIC (POTENTIAL).
TRANSMEM 148 171 4 (POTENTIAL).
DOMAIN 172 178 EXTRACELLULAR (POTENTIAL).
TRANSMEM 179 203 5 (POTENTIAL).
DOMAIN 204 231 CYTOPLASMIC (POTENTIAL).
TRANSMEM 232 257 6 (POTENTIAL).
DOMAIN 258 265 EXTRACELLULAR (POTENTIAL).
TRANSMEM 266 289 7 (POTENTIAL).
DOMAIN 290 >294 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 7 7 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 12 12 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 20 20 N-LINKED (GLCNAC. .) (POTENTIAL).
FT NON_TER 294 294
SQ SEQUENCE 294 AA; 32753 MW; C6ED78FA26B55D42 CRC64;
Query Match 54.38; Score 939; DB 1; Length 294;
Best Local Similarity 63.78; Pred. No. 2.7e-55;
Matches 186; Conservative 40; Mismatches 52; Indels 14; Gaps 4;
QY 26 NASESLGKGYSDGG----CYQLFVSPVEVFTGLVISLLENILVIVAIAKNKLNHSPMYF 81
|||||
7 NATEGNVSQPSVGNTPSPC-EDMGIEVEVFTGLVISLLENILVIGAIARNKLNHVPYF 65
FICSLAVADMVSVNGSETIVITLLNS-----TDTAQSFVTNDVNDVSDVCSLLAS 136
66 FVCSLAVADMVSVLSNSWETITIIYLIANKHLVLDTSVSR----HLDNVFDSMICISLVAS 121
137 ICSSLSTIAVDRYFTFYALQYHNIMTVRRVGIIISCIWAACVTSVGLFIIYSDSSAVIIC 196
122 MCSLLAVADVRYVTFYALRYOHLMTGRCGAIITAGIWTGCGPFIYVYESTYVVCV 181
197 LITMFTTLMALMASLYVHMFLMARLHKRIKRIAVLPGTGTIRQANMKGAITITILIGVYV 256
182 LVAMFLTMLLMSLYAHMFLQARAHVRIIAALPGYRSARQRTSMKGAVTAMLMLGVETV 241
257 CWAPFFHLFIYISCPNQYCVCPMSHFNLYLIMCNSIIDPLIYALRSOE 308
242 CWAPFFHLFIIMISCPNQLYCSPMSHFNLYLIMCNSIIDPLIYALRSOE 293
RESULT 15
MC4R_MOUSE
ID MC4R_MOUSE STANDARD; PRT; 184 AA.
AC P56450;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE Melanocortin-4 receptor (MC4-R) (Fragment).
GN MC4R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Anterior pituitary;
RA Morooka Y., Oomizu S., Takeuchi S., Takahashi S.;
Submitted (DSC-1997) to the EMBL/GenBank/DBJ databases.
-1- FUNCTION: RECEPTOR SPECIFIC TO THE HEPTAPEPTIDE CORE COMMON TO
ADRENOCORTICOTROPIC HORMONE AND ALPHA-, BETA- AND GAMMA-MSH.
THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE
CYCLASE.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-----
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-----
EMBL; AB009664; BAA24015.1; .
MGD; MGI:99457; MC4R.
InterPro: IPR000276; GPCR_Rhodpsn.
Pfam: PF00001; 7tm_1; 1.
PROSITE: PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
PROSITE: PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
phosphorylation; Lipoprotein; Palmitate.
NON_TER 1 1
DOMAIN <1 12 EXTRACELLULAR (POTENTIAL).
TRANSMEM 13 34 3 (POTENTIAL).
DOMAIN 35 54 CYTOPLASMIC (POTENTIAL).
TRANSMEM 55 75 4 (POTENTIAL).
DOMAIN 76 80 EXTRACELLULAR (POTENTIAL).
TRANSMEM 81 104 5 (POTENTIAL).
DOMAIN 105 137 CYTOPLASMIC (POTENTIAL).
TRANSMEM 138 160 6 (POTENTIAL).
DOMAIN 161 169 EXTRACELLULAR (POTENTIAL).
TRANSMEM 170 >184 7 (POTENTIAL).
FT NON_TER 184 184
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SQ SEQUENCE 184 AA; 20614 MW; 9C61CAD31BA0DE33 CRC64;
Query Match 53.9%; Score 932; DB 1; Length 184;
Best Local Similarity 96.7%; Pred. No. 5.1e-55;
Matches 178; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 112 TDAQSTVNIDNVIDSVICSSLLASTCSLLSIADVRYFTFYALQYHNIMTVRRVGIIIS 171
Db 1 TDAQSTVNIDNVIDSVICSSLLASTCSLLSIADVRYFTFYALQYHNIMTVRRVGIIIS 60
QY 172 CIWAAC TVSGVLFIIYSDSSAVIICLIITMFFTMLMASLYVHMFMLMARLHKRIAVLPG 231
Db 61 CIWAAC TVSGVLFIIYSDSSAVIICLIISMFMTMLMASLYVHMFMLMARLHKRIAVLPG 120
QY 232 TGTIRQANMKGAITLTILIGVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLIL 291
Db 121 TGTIRQANMKGAITLTILIGVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLIL 180
QY 292 MCNS 295
Db 181 MCNA 184

Search completed: June 4, 2003, 18:16:17
Job time : 15 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 4, 2003, 18:11:36 ; Search time 52 Seconds
(without alignments)
1315.532 Million cell updates/sec

Title: US-09-884-211A-3
Perfect score: 1728
Sequence: 1 MNSTPHGHMHTSLHFWRNRST.....FKEIICYPGLGLDLSSRY 332

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 205047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriaph.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1657	95.9	332	11 Q9EQM7	Q9eqm7 mus musculus
2	1510.5	87.4	331	13 Q73667	O73667 gallus gall
3	1161.5	67.2	322	13 Q90V73	Q90v73 takifugu po
4	1161.5	67.2	322	13 Q90V70	Q90v70 takifugu ch
5	1156.5	66.9	322	13 Q90V74	Q90v74 takifugu ra
6	1156.5	66.9	322	13 Q90V72	Q90v72 takifugu po
7	1105.5	64.0	325	13 Q73671	O73671 gallus gall
8	1103	63.8	223	6 Q95LB5	Q95lb5 ovis aries
9	1029.5	59.6	325	13 Q93259	Q93259 gallus gall
10	825	47.7	314	13 Q90ZP7	Q90zp7 tangara cuc
11	824	47.7	314	13 Q90V78	Q90v78 coereba fla
12	823	47.6	314	13 Q90ZQ0	Q90zq0 coereba fla
13	823	47.6	314	13 Q90VX9	Q90vx9 coereba fla
14	820	47.5	314	13 Q90ZP8	Q90zp8 coereba fla
15	820	47.5	314	13 Q90V78	Q90v78 coereba fla
16	818	47.3	314	13 Q90ZP9	Q90zp9 coereba fla

17	817	47.3	314	13 Q90W02	Q90w02 coereba fla
18	776.5	44.9	320	6 Q95MM8	Q95mm8 sus scrofa
19	776.5	44.9	233	6 Q95LL18	Q95ll18 sus scrofa
20	771.5	44.6	321	6 Q95KV8	Q95kv8 bos taurus
21	770.5	44.6	317	6 Q8WMC6	Q8wmc6 bos taurus
22	755.5	43.7	317	4 Q8WXX6	Q8wx6 homo sapien
23	754.5	43.7	317	4 Q8WXX6	Q8wx6 homo sapien
24	754.5	43.7	317	4 Q8WXX6	Q8wx6 homo sapien
25	753.5	43.6	317	4 Q96RU4	Q96ru4 homo sapien
26	752.5	43.5	317	6 Q95MP3	Q95mp3 equus cabal
27	751.5	43.5	317	4 Q8WXX7	Q8wx7 homo sapien
28	749.5	43.4	317	4 Q96I33	Q96i33 homo sapien
29	736	42.6	357	13 Q57317	O57317 gallus gall
30	590	34.1	162	6 Q95LB6	Q95lb6 ovis aries
31	570	33.0	221	6 Q9XSH8	Q9xsh8 equus hemio
32	570	33.0	221	6 Q9XSH9	Q9xsh9 equus kiang
33	569	32.9	221	6 Q97660	Q97660 equus zebra
34	569	32.9	221	6 Q9XSH7	Q9xsh7 equus asinu
35	568	32.9	221	6 Q9XSH6	Q9xsh6 equus grevy
36	514.5	29.8	220	6 Q46552	O46552 equus cabal
37	509.5	29.5	220	6 Q9MZA5	Q9mza5 equus cabal
38	435.5	25.2	153	6 Q62814	O62814 sus scrofa
39	367	21.2	364	11 Q88584	O88584 mus musculu
40	366	21.2	366	13 Q9PU17	Q9pu17 xenopus lae
41	366	21.2	366	13 Q9PU16	Q9pu16 xenopus lae
42	338.5	19.6	370	13 Q918K8	Q918k8 brachydanio
43	326	18.9	326	6 Q9BF70	Q9bf70 trichechus
44	326	18.9	326	11 Q99NR8	Q99nr8 castor cana
45	325	18.8	326	6 Q9BF49	Q9bf49 tragelaphus

ALIGNMENTS

RESULT 1

Q9EQM7 PRELIMINARY; PRT; 332 AA.
AC Q9EQM7; DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Melanocortin-4 receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RA Dument L.M., Wu C.S., Mountjoy K.G.;
RT "Characterization of the melanocortin-4 receptor gene.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBD databases.
CC -|- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -|- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF201662; AAG35602.1;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODPSN.
DR PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 332 AA; 36988 MW; 57108415BD424D3 CRC64;

Query Match 95.9%; Score 1657; DB 11; Length 332;
Best Local Similarity 95.5%; Pred. No. 1.1e-137;
Matches 317; Conservative 9; Mismatches 6; Indels 0; Gaps 0;
QY 1 MNSTHHGHMHTSLHFWRNRSTYGPENASLKGYSDDGCGYEQLFVSEVFTLGVISLL 60
DB 1 MNSTHHGHMHTSLHFWRNRSSYGLHNSASLKGKHPDGCYEQLFVSEVFTLGVISLL 60

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QY 61 ENILVIVAIKAKNKLHSPMYFFFCISLAVADMVLSVNSGSETIVITLLNSTDDAQSFVN 120
D 61 ENILVIVAIKAKNKLHSPMYFFFCISLAVADMVLSVNSGSETIVITLLNSTDDAQSFVN 120
QY 121 IDNVDSVICSSLLASICSLSLSTAVDRYFTIFVALQYHNIMTVRRVGGIISCIWAACVTS 180
D 121 IDNVDSVICSSLLASICSLSLSTAVDRYFTIFVALQYHNIMTVRRVGGIISCIWAACVTS 180
QY 181 GVLFIYSDSSAVIICLITMFTMLALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 240
D 181 GVLFIYSDSSAVIICLITMFTMLALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 240
QY 241 MKGATLTILIGVVCWAPFFLHLIFYISCPNYPYCVCFMSHFNYLILIMCNSIIDPL 300
D 241 MKGATLTILIGVVCWAPFFLHLIFYISCPNYPYCVCFMSHFNYLILIMCNSIIDPL 300
QY 301 IYALRSQELRKTFKEIICCYPLGGLCDLSRY 332
D 301 IYALRSQELRKTFKEIICCYPLGGLCDLSRY 332
RESULT 2
073667 PRELIMINARY; PRT; 331 AA.
ID 073667;
AC 073667;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DE Melanocortin 4-receptor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGHORN; TISSUE=LIVER;
RA Takeuchi S., Takahashi S.;
RT "Molecular cloning of the chicken melanocortin 4-receptor gene widely
RT expressed in peripheral tissues.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AB012211; BAA25252.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 331 AA; 36984 MW; 98B25F9A1FFB02C1 CRC64;
Query Match 87.4%; Score 1510.5; DB 13; Length 331;
Best Local Similarity 87.3%; Pred. No. 8.1e-125;
Matches 290; Conservative 15; Mismatches 26; Indels 1; Gaps 1;
QY 1 MNSTHHGHMTSLHFWNRSTYGPNSASLESKGYDGGCYEQLFVSPFVTLGVISLL 60
D 1 MNSTHHGHMTSLHFWNRSTYGPNSASLESKGYDGGCYEQLFVSPFVTLGVISLL 60
QY 1 MNFTQHQRTLOPLHFWNOSN-GLHRGASEPSAKHSGGCGYEQLFVSPFVTLGVISLL 59
D 1 MNFTQHQRTLOPLHFWNOSN-GLHRGASEPSAKHSGGCGYEQLFVSPFVTLGVISLL 59
QY 61 ENILVIVAIKAKNKLHSPMYFFFCISLAVADMVLSVNSGSETIVITLLNSTDDAQSFVN 120
D 61 ENILVIVAIKAKNKLHSPMYFFFCISLAVADMVLSVNSGSETIVITLLNSTDDAQSFVN 119
QY 121 IDNVDSVICSSLLASICSLSLSTAVDRYFTIFVALQYHNIMTVRRVGGIISCIWAACVTS 180
D 121 IDNVDSVICSSLLASICSLSLSTAVDRYFTIFVALQYHNIMTVRRVGGIISCIWAACVTS 179
QY 181 GVLFIYSDSSAVIICLITMFTMLALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 240
D 181 GVLFIYSDSSAVIICLITMFTMLALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 239
QY 241 MKGATLTILIGVVCWAPFFLHLIFYISCPNYPYCVCFMSHFNYLILIMCNSIIDPL 300
D 241 MKGATLTILIGVVCWAPFFLHLIFYISCPNYPYCVCFMSHFNYLILIMCNSIIDPL 300
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Db 240 MKGATLTILIGVVCWAPFFLHLIFYISCPNYPYCVCFMSHFNYLILIMCNSIIDPL 299
QY 301 IYALRSQELRKTFKEIICCYPLGGLCDLSRY 332
D 301 IYALRSQELRKTFKEIICCYPLGGLCDLPCKY 331
RESULT 3
Q90V73 PRELIMINARY; PRT; 322 AA.
ID Q90V73;
AC Q90V73;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Melanocortin receptor-1.
GN MCL1R.
OS Takifugu porphyreus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=176187;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunimoto M., Mizukami Y.;
RT "Discrimination of Takifugu species based on melanocortin receptor-1
RT gene nucleotide sequence.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073677; BAB71733.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35948 MW; A16712C763F91236 CRC64;
Query Match 67.2%; Score 1161.5; DB 13; Length 322;
Best Local Similarity 76.5%; Pred. No. 3.7e-94;
Matches 218; Conservative 31; Mismatches 35; Indels 1; Gaps 1;
QY 36 SDGGCYEQLFVSPFVTLGVISLLENILVIVAIKAKNKLHSPMYFFFCISLAVADMVLSV 95
D 36 SDGGCYEQLFVSPFVTLGVISLLENILVIVAIKAKNKLHSPMYFFFCISLAVADMVLSV 90
QY 96 SNGSETIVITLLNS-TDDAQSFVNIDVNSGICSSLLASICSLSLSTAVDRYFTIFYA 154
D 96 SNGSETIVITLLNS-TDDAQSFVNIDVNSGICSSLLASICSLSLSTAVDRYFTIFYA 150
QY 91 SNASETIVIALINSGTLTIPATLIKSMNDVFDSDMICSSLLASICSLSLSTAVDRYFTIFYA 150
D 91 SNASETIVIALINSGTLTIPATLIKSMNDVFDSDMICSSLLASICSLSLSTAVDRYFTIFYA 150
QY 155 LQYHNIMTVRRVGGIISCIWAACVTSGLVFIYSDSSAVIICLITMFTMLALMASLYVH 214
D 155 LQYHNIMTVRRVGGIISCIWAACVTSGLVFIYSDSSAVIICLITMFTMLALMASLYVH 210
QY 151 LRYHNITVTLRRASLVSISSITWCCTVSGVLFIYVSESTVTLICLITMFTMLALMASLYVH 210
D 151 LRYHNITVTLRRASLVSISSITWCCTVSGVLFIYVSESTVTLICLITMFTMLALMASLYVH 210
QY 215 MFLMARLHKRIAVLPGTGTIRQGANMKGATLTILIGVVCWAPFFLHLIFYISCPON 274
D 215 MFLMARLHKRIAVLPGTGTIRQGANMKGATLTILIGVVCWAPFFLHLIFYISCPON 270
QY 275 PYCVCFMSHFNYLILIMCNSIIDPLIYALRSQELRKTFKEIICC 319
D 275 PYCVCFMSHFNYLILIMCNSIIDPLIYALRSQELRKTFKEIICC 315
RESULT 4
Q90VY0 PRELIMINARY; PRT; 322 AA.
ID Q90VY0;
AC Q90VY0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Melanocortin receptor-1.
GN MCL1R.
OS Takifugu chinensis, and
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=176185, 31033;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=T.chinensis, and F.rubripes;
RA Kunimoto M., Mizukami Y.;
RT "Discrimination of Takifugu species based on melanocortin receptor-1
RT gene nucleotide sequence.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073675; BAB71731.1; -
DR EMBL; AB073674; BAB71730.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35975 MW; 8AF03A6371F5E1F6 CRC64;

Query Match 67.28; Score 1161.5; DB 13; Length 322;
Best Local Similarity 76.58; Pred. No. 3.7e-94;
Matches 218; Conservative 31; Mismatches 35; Indels 1; Gaps 1;

Qy 36 SDGCGYEQLFVSPFVFTLGVISLLENILVIAIAKKNLHSPMYFFICSLAVADMLVSV 95
Db 31 SSTCGYEQMLISTEVFLTLGLIISLLENILVVAIVKKNLHSPMYFFICSLAVADMLVSV 90

Qy 96 SNGSETIVITLLNS-TDTDAOSFTVNDVDSVICSSLLASICSLLSIADVRYTIFYA 154
Db 91 SNASETIVIALINSGLTIPATLIKSDMNVFDSMICSSLLASICSLLAIADVRYTIFYA 150

Qy 155 LOYHNIMTVRVGIIISCIWAACVSGVLFIYSDSSAVIICLTIMFTMLMASLVVH 214
Db 151 LRYHNIVTLRRASLVSIISWTCCTVSGVLFIYSESTVLCITIMFTMLMASLVVH 210

Qy 215 MFLMARLHKRIAVLPGTGTIRQGANMKGAITLTILIGVVFVVCWAPFFLHLIFYISCPON 274
Db 211 MFLARLHKRIEAMPGNAPHORANLKGAITLTILIGVVFVVCWAPFFLHLITMTCPN 270

Qy 275 PYCVFMSHFNLYLILIMCNSIIDPLIYALRSQELRTFKEIICC 319
Db 271 PYCTCFMSHFNMYLILIMCNSVIDPIIYAFRSQEMRKTFKEIFCC 315

RESULT 5
Q90Y74 PRELIMINARY; PRT; 322 AA.
ID Q90Y74;
AC Q90Y74;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Melanocortin receptor-1.
GN MC1R.
OS Takifugu radiatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=176186;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunimoto M., Mizukami Y.;
RT "Discrimination of Takifugu species based on melanocortin receptor-1
RT gene nucleotide sequence.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073676; BAB71732.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35917 MW; 37A8339FDCD84C38 CRC64;
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Query Match 66.98; Score 1156.5; DB 13; Length 322;
Best Local Similarity 76.18; Pred. No. 1e-93;
Matches 217; Conservative 31; Mismatches 36; Indels 1; Gaps 1;

Qy 36 SDGCGYEQLFVSPFVFTLGVISLLENILVIAIAKKNLHSPMYFFICSLAVADMLVSV 95
Db 31 SSTCGYEQMLISTEVFLTLGLIISLLENILVVAIVKKNLHSPMYFFICSLAVADMLVSV 90

Qy 96 SNGSETIVITLLNS-TDTDAOSFTVNDVDSVICSSLLASICSLLSIADVRYTIFYA 154
Db 91 SNASETIVIALINSGLTIPATLIKSDMNVFDSMICSSLLASICSLLAIADVRYTIFYA 150

Qy 155 LOYHNIMTVRVGIIISCIWAACVSGVLFIYSDSSAVIICLTIMFTMLMASLVVH 214
Db 151 LRYHNIVTLRRASLVSIISWTCCTVSGVLFIYSESTVLCITIMFTMLMASLVVH 210

Qy 215 MFLMARLHKRIAVLPGTGTIRQGANMKGAITLTILIGVVFVVCWAPFFLHLIFYISCPON 274
Db 211 MFLARLHKRIEAMPGNAPHORANLKGAITLTILIGVVFVVCWAPFFLHLITMTCPN 270

Qy 275 PYCVFMSHFNLYLILIMCNSIIDPLIYALRSQELRTFKEIICC 319
Db 271 PYCTCFMSHFNMYLILIMCNSVIDPIIYAFRSQEMRKTFKEIFCC 315

RESULT 6
Q90Y72 PRELIMINARY; PRT; 322 AA.
ID Q90Y72;
AC Q90Y72;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Melanocortin receptor-1.
GN MC1R.
OS Takifugu poecilognotus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=176188;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunimoto M., Mizukami Y.;
RT "Discrimination of Takifugu species based on melanocortin receptor-1
RT gene nucleotide sequence.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073678; BAB71734.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35945 MW; 1C3F1B3BCED4BFF8 CRC64;

Query Match 66.98; Score 1156.5; DB 13; Length 322;
Best Local Similarity 76.18; Pred. No. 1e-93;
Matches 217; Conservative 31; Mismatches 36; Indels 1; Gaps 1;

Qy 36 SDGCGYEQLFVSPFVFTLGVISLLENILVIAIAKKNLHSPMYFFICSLAVADMLVSV 95
Db 31 SSTCGYEQMLISTEVFLTLGLIISLLENILVVAIVKKNLHSPMYFFICSLAVADMLVSV 90

Qy 96 SNGSETIVITLLNS-TDTDAOSFTVNDVDSVICSSLLASICSLLSIADVRYTIFYA 154
Db 91 SNASETIVIALINSGLTIPATLIKSDMNVFDSMICSSLLASICSLLAIADVRYTIFYA 150

Qy 155 LOYHNIMTVRVGIIISCIWAACVSGVLFIYSDSSAVIICLTIMFTMLMASLVVH 214
Db 151 LRYHNIVTLRRASLVSIISWTCCTVSGVLFIYSESTVLCITIMFTMLMASLVVH 210

Qy 215 MFLMARLHKRIAVLPGTGTIRQGANMKGAITLTILIGVVFVVCWAPFFLHLIFYISCPON 274
Db 211 MFLARLHKRIEAMPGNAPHORANLKGAITLTILIGVVFVVCWAPFFLHLITMTCPN 270
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KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 325 AA; 36601 MW; 94FA631ED144C17 CRC64;

Query Match
Best Local Similarity 61.6%; Score 1029.5; DB 13; Length 325;
Matches 202; Conservative 41; Mismatches 62; Indels 23; Gaps 4;

QY 1 MNSTHHGMHTSLFHWNRSTYGP-----HSNASESLGKGYSDGGCYEQLFVSPEVFTLG 55
DB 1 MNSTHF-----TFSPQVLLNVTEDISDILNRRSSDGFCEQVFKAEVFTLG 49
QY 56 VISLEENILVATAKKNLHSPMYFFICSLAVADMVLSVNGSETIVITLLNS-----TD 111
DB 50 IISLMENILVIALKGNLHSPMYFFICSLAVADMVLSVNGSETIVITLLNS-----TD 111
QY 112 TDAQSFVNIDNVDSVICSLLASIGLSIADVRFETIFYALQYHNMIVRRVGIIS 171
DB 110 ---DHFTQHDNVFDSMICSILVASICNLLVIAIDRYITIFYALYHSIMTVKRALTLIV 166
QY 172 CIWAACVSGYLFIIYSDSSAVIICLITMFTMLMALMASLYVHMFMLARLHKRIAVLPG 231
DB 167 LIWISCIIGIIFAYSESKTVIVCLITMFTMLFLMASLYVHMFMLARLHKRIALPV 226
QY 232 TGTTRQGANMKGATITILIGVFCVWAPPLHLIFYISCPNQYCVCFMSHFNLYILI 291
DB 227 DGVPSQRTCKMGATITITLLGVFCVWAPPLHLILIIISCPMPYCVCYTSHFNLYILI 286
QY 292 MCNSIIDPLIYALRSOELRKTFTIC 319
DB 287 MCNSVIDPLIYAFRSLEMRKTFTKEIVCC 314

RESULT 10
Q902P7 PRELIMINARY; PRT; 314 AA.
AC Q902P7:
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Melanocortin 1 receptor.
OS Tangara cucullata.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Passeroidea;
OC Fringillidae; Emberizinae; Tangara.
OX NCBI_TaxID=158457;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21261843; PubMed=11369199;
RA Theron E., Hawkins K., Bermingham E., Ricklefs R.E., Mundy N.I.;
RT "The molecular basis of an avian plumage polymorphism in the wild: a
RT melanocortin-1-receptor point mutation is perfectly associated with
RT the melanic plumage morph of the bananaquit, Coereba flaveola."
RL Curr. Biol. 11:550-557(2001).
DR EMBL; AF362600; AAK50807.1; -
DR EMBL; AF362575; AAK50782.1; -
DR EMBL; AF362576; AAK50783.1; -
DR EMBL; AF362577; AAK50784.1; -
DR EMBL; AF362579; AAK50786.1; -
DR EMBL; AF362580; AAK50787.1; -
DR EMBL; AF362581; AAK50788.1; -
DR EMBL; AF362582; AAK50789.1; -
DR EMBL; AF362585; AAK50792.1; -
DR EMBL; AF362587; AAK50794.1; -
DR EMBL; AF362588; AAK50795.1; -
DR EMBL; AF362589; AAK50796.1; -
DR EMBL; AF362590; AAK50797.1; -
DR EMBL; AF362591; AAK50798.1; -
DR EMBL; AF362592; AAK50799.1; -
DR EMBL; AF362593; AAK50800.1; -
DR EMBL; AF362594; AAK50801.1; -
DR EMBL; AF362595; AAK50802.1; -
DR EMBL; AF362596; AAK50803.1; -
DR EMBL; AF362597; AAK50804.1; -
DR EMBL; AF362598; AAK50805.1; -
DR EMBL; AF362599; AAK50806.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 314 AA; 35015 MW; ACB246930C38DDB9 CRC64;

Query Match
Best Local Similarity 51.0%; Score 825; DB 13; Length 314;
Matches 155; Conservative 62; Mismatches 81; Indels 6; Gaps 2;

QY 17 NRSTYGPNSHNASISLGKGYSDGGCYEQLFVSPEVFTLGIVISLLENILVIAIKNNLH 76
DB 14 SNASEGNSHNASISLGKGYSDGGCYEQLFVSPEVFTLGIVISLLENILVIAIKNNLH 68
QY 77 SPWYFFICSCLAVADMVLSVNGSETIVITLL-NTDQSFVNIDNVDSVICSLLA 135
DB 69 SPTYFFICCLAVSDMLVSISLAEMFLMLLEHGVLMVRPISVIRHMSVIDTLCSSVFS 128
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QY 136 SICLLSIAVDRTYFTIFYALQYHNMIVRRVGIISCIWAACVSGYLFIIYSDSSAVII 195
DB 129 SLSFLGVIAVDRTYFTIFYALQYHNMIVRRVGIISCIWAACVSGYLFIIYSDSSAVII 188
QY 196 CLIMTEFFMLMALMASLYVHMFMLARLHKRIAVLPGTGTIRQGANMKGATITILIGVFCV 255
DB 189 CLIGFFELFMLVLMVLIYHMFALARHHLHSISQOKPPTAHRGSLGKAVTLITLLGVFF 248
QY 256 VCMAPFFLHLIFYISCPNQYCVCFMSHFNLYILIMCNSIIDPLIYALRSOELRKTFTKE 315
DB 249 ICWGPFFHLLIIVTCPTNPCTCFEFSYFNFLILIIICNSVIDPLIYAFRSOELRKTRE 308
QY 316 IICC 319
DB 309 VVTC 312

RESULT 11
Q90VV8 PRELIMINARY; PRT; 314 AA.
AC Q90VV8:
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Melanocortin 1 receptor.
OS Coereba flaveola (bananaquit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Passeroidea;
OC Fringillidae; Emberizinae; Coereba.
OX NCBI_TaxID=87177;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21261843; PubMed=11369199;
RA Theron E., Hawkins K., Bermingham E., Ricklefs R.E., Mundy N.I.;
RT "The molecular basis of an avian plumage polymorphism in the wild: a
RT melanocortin-1-receptor point mutation is perfectly associated with
RT the melanic plumage morph of the bananaquit, Coereba flaveola."
RL Curr. Biol. 11:550-557(2001).
DR EMBL; AF362600; AAK50807.1; -
DR EMBL; AF362575; AAK50782.1; -
DR EMBL; AF362576; AAK50783.1; -
DR EMBL; AF362577; AAK50784.1; -
DR EMBL; AF362579; AAK50786.1; -
DR EMBL; AF362580; AAK50787.1; -
DR EMBL; AF362581; AAK50788.1; -
DR EMBL; AF362582; AAK50789.1; -
DR EMBL; AF362585; AAK50792.1; -
DR EMBL; AF362587; AAK50794.1; -
DR EMBL; AF362588; AAK50795.1; -
DR EMBL; AF362589; AAK50796.1; -
DR EMBL; AF362590; AAK50797.1; -
DR EMBL; AF362591; AAK50798.1; -
DR EMBL; AF362592; AAK50799.1; -
DR EMBL; AF362593; AAK50800.1; -
DR EMBL; AF362594; AAK50801.1; -
DR EMBL; AF362595; AAK50802.1; -
DR EMBL; AF362596; AAK50803.1; -
DR EMBL; AF362597; AAK50804.1; -
DR EMBL; AF362598; AAK50805.1; -
DR EMBL; AF362599; AAK50806.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 314 AA; 35008 MW; CB704F205AB3C556 CRC64;

Query Match
Best Local Similarity 47.7%; Score 824; DB 13; Length 314;
Matches 154; Conservative 64; Mismatches 80; Indels 6; Gaps 2;

QY 17 NRSTYGPNSHNASISLGKGYSDGGCYEQLFVSPEVFTLGIVISLLENILVIAIKNNLH 76
DB 14 SNASEGNSHNASISLGKGYSDGGCYEQLFVSPEVFTLGIVISLLENILVIAIKNNLH 68
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Db 14 SNAEGHNSNATVAGGWCQ-----LDIPNELFLALGLVSLVENLLVVAAILKRNHL 68
QY 77 SPMYFFICSLAVADMLVSVNGSETIVITLL-NSTDQDAQSFVNIDNVIDSVICSSLLA 135
Db 69 SPTYFFICCLAVSDMLVSVISNLAEMFLMLLLEHGLVLMRPSIVRHMSVDITLICSSVVS 128
QY 136 SICSLLSIAVDRTFTFYALQYHNIMTVRRVGIISCIWAACVSGVLFIYSDSSAVII 195
Db 129 SLSEFLGVIAVDRTFTFYALRYHSIMTLQRAVVTMAVSLASTVSVTLIAYRSNTILL 188
QY 196 CLITMEFTMLALMASLYVHMTLMARLHKRIKRAVLPCTGTIRGANNKMGAITLILGVFV 255
Db 189 CLIGFLFMLVLMVLYIHMFLARHLHSHISSQQPPTAHRGSLKGAVTTLILGVFF 248
QY 256 VCMAPFFHLFIYISCPQNPYCVCFMSHFNLIILIMCNSIIDPLIYALRSQELRKTKE 315
Db 249 ICWGPEFFHLILIVTCPTNPFACFFSYFNFLIILICNSVIDPLIYAFRSQELRLTRE 308
QY 316 IICC 319
Db 309 VVTC 312

RESULT 12

Q90200 ID Q90200 PRELIMINARY; PRT; 314 AA.
AC Q90200
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Melanocortin 1 receptor.
OS Coereba flaveola (banaquit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Passeroidea;
OC Fringillidae; Emberizinae; Coereba.
OX NCBI_TaxID=87177;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21261843; PubMed=11369199;
RA Theron E., Hawkins K., Birmingham E., Ricklefs R.E., Mundy N.I.;
RT "The molecular basis of an avian plumage polymorphism in the wild: a
RT melanocortin-1-receptor point mutation is perfectly associated with
RT the melanic plumage morph of the bananaquit, Coereba flaveola."
RL Curr. Biol. 11:550-557(2001).
DR EMBL; AF362584; AAK50791.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 314 AA; 34998 MW; 2174CD2BE615BAEB CRC64;

Query Match 47.6%; Score 823; DB 13; Length 314;
Best Local Similarity 50.3%; Pred. No. 2e-64;
Matches 153; Conservative 65; Mismatches 80; Indels 6; Gaps 2;

QY 17 NRSTYGPISNASESLGKYGCGVEQFLVSPVFTVLGVLISLLENILVIVAIAKKNLH 76
Db 14 SNAEGHNSNATVAGGWCQ-----LDIPNELFLALGLVSLVENLLVVAAILKRNHL 68
QY 77 SPMYFFICSLAVADMLVSVNGSETIVITLL-NSTDQDAQSFVNIDNVIDSVICSSLLA 135
Db 69 SPTYFFICCLAVSDMLVSVISNLAEMFLMLLLEHGLVLMRPSIVRHMSVDITLICSSVVS 128
QY 136 SICSLLSIAVDRTFTFYALQYHNIMTVRRVGIISCIWAACVSGVLFIYSDSSAVII 195
Db 129 SLSEFLGVIAVDRTFTFYALRYHSIMTLQRAVVTMAVSLASTVSVTLIAYRSNTILL 188
QY 196 CLITMEFTMLALMASLYVHMTLMARLHKRIKRAVLPCTGTIRGANNKMGAITLILGVFV 255
Db 189 CLIGFLFMLVLMVLYIHMFLARHLHSHISSQQPPTAHRGSLKGAVTTLILGVFF 248
QY 256 VCMAPFFHLFIYISCPQNPYCVCFMSHFNLIILIMCNSIIDPLIYALRSQELRKTKE 315

Db 249 ICWGPEFFHLILIVTCPTNPFACFFSYFNFLIILICNSVIDPLIYAFRSQELRLTRE 308
QY 316 IICC 319
Db 309 VVTC 312

RESULT 13

Q90VX9 ID Q90VX9 PRELIMINARY; PRT; 314 AA.
AC Q90VX9
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Melanocortin 1 receptor.
OS Coereba flaveola (banaquit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Passeroidea;
OC Fringillidae; Emberizinae; Coereba.
OX NCBI_TaxID=87177;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21261843; PubMed=11369199;
RA Theron E., Hawkins K., Birmingham E., Ricklefs R.E., Mundy N.I.;
RT "The molecular basis of an avian plumage polymorphism in the wild: a
RT melanocortin-1-receptor point mutation is perfectly associated with
RT the melanic plumage morph of the bananaquit, Coereba flaveola."
RL Curr. Biol. 11:550-557(2001).
DR EMBL; AF362583; AAK50790.1; -
DR EMBL; AF362578; AAK50785.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 314 AA; 35024 MW; 8BDA7D205AA4675A CRC64;

Query Match 47.6%; Score 823; DB 13; Length 314;
Best Local Similarity 50.3%; Pred. No. 2e-64;
Matches 153; Conservative 65; Mismatches 80; Indels 6; Gaps 2;

QY 17 NRSTYGPISNASESLGKYGCGVEQFLVSPVFTVLGVLISLLENILVIVAIAKKNLH 76
Db 14 SNAEGHNSNATVAGGWCQ-----LDIPNELFLALGLVSLVENLLVVAAILKRNHL 68
QY 77 SPMYFFICSLAVADMLVSVNGSETIVITLL-NSTDQDAQSFVNIDNVIDSVICSSLLA 135
Db 69 SPTYFFICCLAVSDMLVSVISNLAEMFLMLLLEHGLVLMRPSIVRHMSVDITLICSSVVS 128
QY 136 SICSLLSIAVDRTFTFYALQYHNIMTVRRVGIISCIWAACVSGVLFIYSDSSAVII 195
Db 129 SLSEFLGVIAVDRTFTFYALRYHSIMTLQRAVVTMAVSLASTVSVTLIAYRSNTILL 188
QY 196 CLITMEFTMLALMASLYVHMTLMARLHKRIKRAVLPCTGTIRGANNKMGAITLILGVFV 255
Db 189 CLIGFLFMLVLMVLYIHMFLARHLHSHISSQQPPTAHRGSLKGAVTTLILGVFF 248
QY 256 VCMAPFFHLFIYISCPQNPYCVCFMSHFNLIILIMCNSIIDPLIYALRSQELRKTKE 315
Db 249 ICWGPEFFHLILIVTCPTNPFACFFSYFNFLIILICNSVIDPLIYAFRSQELRLTRE 308
QY 316 IICC 319
Db 309 VVTC 312

RESULT 14

Q902P8 ID Q902P8 PRELIMINARY; PRT; 314 AA.
AC Q902P8
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)


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DR EMBL; AF362603; AAK50810.1; -
DR EMBL; AF362601; AAK50808.1; -
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
DR Receptor. KW
SQ SEQUENCE 314 AA; 35037 MW; 666E3AA712D7409C CRC64;

Query Match          47.5%; Score 820; DB 13; Length 314;
Best Local Similarity 50.3%; Pred. No. 3.7e-64;
Matches 133; Conservative 65; Mismatches 80; Indels 6; Gaps 2;

QY   17 NRSTYGPHNASESLGKGYSDGGCYEQLFVSPVFVTGLGVISLENIILVIAAKNNLH 76
Db    : : | ||| : | : | : | : | : | : | : | : | : | : | : | : | : |
      14 SNAEGNHSNATVGAGGWCQG----LDIPNELFLALGLVSLVENLLVVAAILKNRNLH 68

QY   77 SPMYFFICSLAYADMLVSVNSGETIVITLL-NSTDDAQSFVNINDVIDSVCSSLA 135
Db    || |||| |||| |||| || : : : | : | : | : | : | : | : | : | : | : | : |
      69 SPYYFIFCLVASDMLVSIISNLAKMFLMLELHGVLVMRPISVRHMDSVIDTLICSSWS 128

QY   136 SICLSLSIADVFTTFYALQYHNIMTVRRVGIIISCIWAACTVSGVLFTIYSDSAVII 195
Db    | : | |||| |||| |||| |||| : : : | : | : | : | : | : | : | : | : |
      129 SLNFLGVIADVTTTFYALRYHSIMTQLQAVVTMASVWLASTVSTLTITYRSNTILL 188

QY   196 CLITMFTTMLAMASLYVMFMARLHIKRIAVLPGTGITIQGANMKGATLLILIGVFV 255
Db    ||| | | | | | | | | | | | | | : | : | : | : | : | : | : | : | : |
      189 CLIGFFLFMLVLMVLVLIHMFALEARHLHSISSQQKPPTAHRGSGSLKGAVTLTLLGVFF 248

QY   256 VCWAPEFLHLIFYSQPQNPYCVCMFNSHENLXLLIMCNSIDPLIALYRSQELRKTFKE 315
Db    ||| | | | | | : | | | | | | | | : | : | : | : | : | : | : | : | : |
      249 ICMPGPFHHLLIVTCPTPCFCFFSYFNLFLLILICNSVIDPLIYAFRSQELRLTLE 308

QY   316 IIQC 319
Db    : : |

QY   309 VUTC 312

Search completed: June 4, 2003, 18:18:09
Job time : 54 secs

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Db 61 ENILVIVAIAKNNKLNHSPMYFFTCISLAVADMLVSVNGSETHIIITLLNSTDTDAQSFTVN 120
QY 121 IDNVDSVICSSLLASICSLSIAVDRTYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
121 IDNVDSVICSSLLASICSLSIAVDRTYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
Db 121 IDNVDSVICSSLLASICSLSIAVDRTYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
QY 181 GILFIYSDSTAVIICLITMFFTMLALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 240
181 GILFIYSDSTAVIICLITMFFTMLALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 240
Db 181 GILFIYSDSTAVIICLITMFFTMLALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 240
QY 241 MKGAITLTILIGVYVVCWAPFFLHLFIYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
241 MKGAITLTILIGVYVVCWAPFFLHLFIYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
Db 241 MKGAITLTILIGVYVVCWAPFFLHLFIYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
QY 301 IYALRSQELRKTKEIICCYPLGGLCDLSRY 332
301 IYALRSQELRKTKEIICCYPLGGLCDLSRY 332
Db 301 IYALRSQELRKTKEIICCYPLGGLCDLSRY 332

RESULT 2

US-08-672-109B-8
; Sequence 8, Application US/08672109B
; Patent No. 5710265
; GENERAL INFORMATION:
; APPLICANT: Yamada, Tadataka
; APPLICANT: Gantz, Ira
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: US
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,109B
; FILING DATE: June 27, 1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Deann F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-000853DVC
; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-672-109B-8

Query Match 94.9%; Score 1638.5; DB 1; Length 332;
Best Local Similarity 95.5%; Pred. No. 4.8e-126;
Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;
QY 1 MNSTLQHGHTSLHFWNRSTYQHGHNATESLGKGYDGGCYBQLFVSPFVTLGVISLL 60
121 IDNVDSVICSSLLASICSLSIAVDRTYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
Db 121 IDNVDSVICSSLLASICSLSIAVDRTYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
QY 61 ENILVIVAIAKNNKLNHSPMYFFTCISLAVADMLVSVNGSETHIIITLLNSTDTDAQSFTVN 120
61 ENILVIVAIAKNNKLNHSPMYFFTCISLAVADMLVSVNGSETHIIITLLNSTDTDAQSFTVN 120
Db 61 ENILVIVAIAKNNKLNHSPMYFFTCISLAVADMLVSVNGSETHIIITLLNSTDTDAQSFTVN 120
QY 121 IDNVDSVICSSLLASICSLSIAVDRTYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
121 IDNVDSVICSSLLASICSLSIAVDRTYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
Db 121 IDNVDSVICSSLLASICSLSIAVDRTYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
QY 121 IDNVDSVICSSLLASICSLSIAVDRTYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180

Db 121 IDNVDSVICSSLLASICSLSIAVDRTYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
QY 181 GILFIYSDSTAVIICLITMFFTMLALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 240
181 GILFIYSDSTAVIICLITMFFTMLALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 240
Db 181 GILFIYSDSTAVIICLITMFFTMLALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 240
QY 241 MKGAITLTILIGVYVVCWAPFFLHLFIYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
241 MKGAITLTILIGVYVVCWAPFFLHLFIYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
Db 241 MKGAITLTILIGVYVVCWAPFFLHLFIYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
QY 301 IYALRSQELRKTKEIICCYPLGGLCDLSRY 332
301 IYALRSQELRKTKEIICCYPLGGLCDLSRY 332
Db 301 IYALRSQELRKTKEIICCYPLGGLCDLSRY 332

RESULT 3

US-08-842-045-8
; Sequence 8, Application US/08842045
; Patent No. 5817787
; GENERAL INFORMATION:
; APPLICANT: Yamada, Tadataka
; APPLICANT: Gantz, Ira
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: US
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842,045
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Deann F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-000853DVE
; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-842-045-8

Query Match 94.9%; Score 1638.5; DB 2; Length 332;
Best Local Similarity 95.5%; Pred. No. 4.8e-126;
Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;
QY 1 MNSTLQHGHTSLHFWNRSTYQHGHNATESLGKGYDGGCYBQLFVSPFVTLGVISLL 60
121 IDNVDSVICSSLLASICSLSIAVDRTYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
Db 121 IDNVDSVICSSLLASICSLSIAVDRTYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
QY 61 ENILVIVAIAKNNKLNHSPMYFFTCISLAVADMLVSVNGSETHIIITLLNSTDTDAQSFTVN 120
61 ENILVIVAIAKNNKLNHSPMYFFTCISLAVADMLVSVNGSETHIIITLLNSTDTDAQSFTVN 120
Db 61 ENILVIVAIAKNNKLNHSPMYFFTCISLAVADMLVSVNGSETHIIITLLNSTDTDAQSFTVN 120
QY 121 IDNVDSVICSSLLASICSLSIAVDRTYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
121 IDNVDSVICSSLLASICSLSIAVDRTYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
Db 121 IDNVDSVICSSLLASICSLSIAVDRTYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
QY 181 GILFIYSDSTAVIICLITMFFTMLALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 240
181 GILFIYSDSTAVIICLITMFFTMLALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 240
Db 181 GILFIYSDSTAVIICLITMFFTMLALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 240

Db 181 MGKAITLILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 240
Qy 241 MGKAITLILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
Db 241 MGKAITLILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
Qy 301 IYALRSQELRKTKEIKICCPYGLGCLDLSRY 332
Db 301 IYALRSQELRKTKEIKICCPYGLGCLDLSRY 332

RESULT 4
US-08-842-238-8
; Sequence 8, Application US/08842238
; Patent No. 5869257
; GENERAL INFORMATION:
; APPLICANT: Yamada, Tadataka
; APPLICANT: Gantz, Ira
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: US
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842,238
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, DeAnn F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-000853DVD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-842-238-8

Query Match 94.9%; Score 1638.5; DB 2; Length 332;
Best Local Similarity 95.5%; Pred. No. 4.8e-126;
Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;
Qy 1 MNSTLQHGMTSLHFVNRSTYGOHGNATESLGRKYPDGGCYEQLFVSPVEVTLGVLSLL 60
Db 2 VNST-HRGMHTSLHLNRSYRLHSNASESLGRKYSDDGCYEQLFVSPVEVTLGVLSLL 60
Qy 61 ENILVIVIAAKNKLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
Db 61 ENILVIVIAAKNKLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
Qy 121 IDNVDSVICSLLASCSLLSSTAVDRYFTIFALQYHNMTVRRVGIISCIWAACVTS 180
Db 121 IDNVDSVICSLLASCSLLSSTAVDRYFTIFALQYHNMTVRRVGIISCIWAACVTS 180
Qy 181 GILFIYSDSTAVTICLITMFFTMALMASLYVHMFMLARHLKRIAVLPCTGTIROGAN 240
Db 181 GILFIYSDSVAIICLITMFFTMALMASLYVHMFMLARHLKRIAVLPCTGTIROGAN 240
Qy 241 MGKAITLILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300

Db 241 MGKAITLILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
Qy 301 IYALRSQELRKTKEIKICCPYGLGCLDLSRY 332
Db 301 IYALRSQELRKTKEIKICCPYGLGCLDLSRY 332

RESULT 5
US-08-780-749A-2
; Sequence 2, Application US/08780749A
; Patent No. 5932779
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank
; APPLICANT: Huszar, Dennis
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS
; TITLE OF INVENTION: USEFUL IN THE REGULATION OF BODY WEIGHT
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,749A
; FILING DATE: 08-JAN-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Laura A. Coruzzi
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-780-749A-2

Query Match 94.9%; Score 1638.5; DB 2; Length 332;
Best Local Similarity 95.5%; Pred. No. 4.8e-126;
Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;
Qy 1 MNSTLQHGMTSLHFVNRSTYGOHGNATESLGRKYPDGGCYEQLFVSPVEVTLGVLSLL 60
Db 2 VNST-HRGMHTSLHLNRSYRLHSNASESLGRKYSDDGCYEQLFVSPVEVTLGVLSLL 60
Qy 61 ENILVIVIAAKNKLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
Db 61 ENILVIVIAAKNKLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
Qy 121 IDNVDSVICSLLASCSLLSSTAVDRYFTIFALQYHNMTVRRVGIISCIWAACVTS 180
Db 121 IDNVDSVICSLLASCSLLSSTAVDRYFTIFALQYHNMTVRRVGIISCIWAACVTS 180
Qy 181 GILFIYSDSTAVTICLITMFFTMALMASLYVHMFMLARHLKRIAVLPCTGTIROGAN 240
Db 181 GILFIYSDSVAIICLITMFFTMALMASLYVHMFMLARHLKRIAVLPCTGTIROGAN 240
Qy 241 MGKAITLILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300

Db 241 MKGATITLILGVVVCWAPFFLHLIFYISCPQNPVCVCFMSHFNLYLILMCNSIIDPL 300

QY 301 IYALRSQELRKTFKEIICCYPLGGLCDLSSRY 332
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Db 301 IYALRSQELRKTFKEIICCYPLGGLCDLSSRY 332

RESULT 6
US-08-629-335B-8
; Sequence 8, Application US/08629335B
; Patent No. 6117975
; GENERAL INFORMATION:
; APPLICANT: Yamada, Tadataka
; APPLICANT: Gantz, Ira
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: US
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/629,335B
; FILING DATE: July 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Deann F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-000853DVA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-629-335B-8

Query Match 94.9%; Score 1638.5; DB 3; Length 332;
Best Local Similarity 95.5%; Pred. No. 4.8e-126;
Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 1 MNSTLQHGHTSLHFWNRSTYGOHGNATESLKGYPDGGCYEQOLFVSPVEFVTLGVISLL 60
:|||||

Db 2 VNST-HRGMHTSLHLNRSYRLHNSASESLGKGYSDGGCYEQOLFVSPVEFVTLGVISLL 60
:|||||

QY 61 ENILVIVATAKNKLNHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
:|||||

Db 61 ENILVIVATAKNKLNHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
:|||||

QY 121 IDNVDSVICSSLLASICSLLSIADVDRTYFYALQYHNIMTVRRVGGIIISCIWAACVTS 180
:|||||

Db 121 IDNVDSVICSSLLASICSLLSIADVDRTYFYALQYHNIMTVRRVGGIIISCIWAACVTS 180
:|||||

QY 181 GILFIYSDSTAVIICLTIMFTMLMALMASLVHMFMLARLHKRIAVLPGTGTIRQGAN 240
:|||||

Db 181 GILFIYSDSSAVIICLTIMFTMLMALMASLVHMFMLARLHKRIAVLPGTGTIRQGAN 240
:|||||

QY 241 MKGATITLILGVVVCWAPFFLHLIFYISCPQNPVCVCFMSHFNLYLILMCNSIIDPL 300
:|||||

Db 241 MKGATITLILGVVVCWAPFFLHLIFYISCPQNPVCVCFMSHFNLYLILMCNSIIDPL 300
:|||||

QY 301 IYALRSQELRKTFKEIICCYPLGGLCDLSSRY 332
|||||

Db 301 IYALRSQELRKTFKEIICCYPLGGLCDLSSRY 332

RESULT 8
US-09-384-302A-9
; Sequence 9, Application US/09384302A
; Patent No. 6451543
; GENERAL INFORMATION:
; APPLICANT: Kochendoerfer, Gerd G
; APPLICANT: Hunter, Christie L
; APPLICANT: Kent, Stephen B.H.
; APPLICANT: Botti, Paolo
; APPLICANT: Gryphon Sciences
; TITLE OF INVENTION: Lipid Matrix-Assisted Chemical Ligation and Synthesis
; FILE REFERENCE: of Membrane Polypeptides
; CURRENT APPLICATION NUMBER: US/09/384,302A
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: 09/144,964
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 09/263,971
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 30


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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-780-749A-6

Query Match          94.6%; Score 1632.5; DB 2; Length 332;
Best Local Similarity 95.2%; Pred. No. 1.5e-125;
Matches 316; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

QY 1 MNSTLQHGHTSLHFNRSTYGOHGNATESLGKGYPDGGCYEQLFVSPFVTLGVISLL 60
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
QY 2 VNST-HRGHTSLHLNRRSSYRLHNSASESLGKGYSDGGCYEQLFVSPFVTLGVISLL 60
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
QY 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
QY 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
QY 121 IDNVDSVICSSLLASICSLLSIADVRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
QY 121 IDNVDSVICSSLLASICSLLSIADVRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
QY 181 GILFIYSDSTAVIICLTIMFTTMLALMASLVVHMFMLARLHKRIAVLPGTGTIROGAN 240
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
QY 181 GILFIYSDSTAVIICLTIMFTTMLALMASLVVHMFMLARLHKRIAVLPGTGTIROGAN 240
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
QY 241 MKGATITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMNCNSIIDPL 300
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
QY 301 IYALRSQELRKTFKEIICCYPLGGCLDLSRY 332
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
QY 301 IYALRSQELRKTFKEIICCYPLGGCLDLSRY 332
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||

RESULT 11
US-08-870-511-6
; Sequence 6, Application US/08870511
; Patent No. 6287763
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank
; APPLICANT: Huszar, Dennis
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE
; TITLE OF INVENTION: REGULATION OF BODY WEIGHT
; FILE REFERENCE: 7853-083
; CURRENT APPLICATION NUMBER: US/08/870,511
; CURRENT FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-870-511-6

Query Match          94.3%; Score 1627.5; DB 4; Length 332;
Best Local Similarity 94.9%; Pred. No. 3.8e-125;
Matches 315; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 MNSTLQHGHTSLHFNRSTYGOHGNATESLGKGYPDGGCYEQLFVSPFVTLGVISLL 60
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
QY 2 VNST-HRGHTSLHLNRRSSYRLHNSASESLGKGYSDGGCYEQLFVSPFVTLGVISLL 60
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
QY 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
QY 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
QY 121 IDNVDSVICSSLLASICSLLSIADVRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
QY 121 IDNVDSVICSSLLASICSLLSIADVRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
QY 181 GILFIYSDSTAVIICLTIMFTTMLALMASLVVHMFMLARLHKRIAVLPGTGTIROGAN 240
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
QY 181 GILFIYSDSTAVIICLTIMFTTMLALMASLVVHMFMLARLHKRIAVLPGTGTIROGAN 240
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
QY 241 MKGATITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMNCNSIIDPL 300
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
QY 241 MKGATITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMNCNSIIDPL 300
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
QY 301 IYALRSQELRKTFKEIICCYPLGGCLDLSRY 332
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
QY 301 IYALRSQELRKTFKEIICCYPLGGCLDLSRY 332
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||

RESULT 13
US-08-870-511-10
; Sequence 10, Application US/08870511
; Patent No. 6287763
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```
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank
; APPLICANT: Huszar, Dennis
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE
; TITLE OF INVENTION: REGULATION OF BODY WEIGHT
; FILE REFERENCE: 7853-083
; CURRENT APPLICATION NUMBER: US/08/870,511
; CURRENT FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-870-511-10

Query Match          94.2%; Score 1626.5; DB 4; Length 332;
Best Local Similarity 94.9%; Pred. No. 4.6e-125;
Matches 315; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 MNSTLQHCWHTSLHFWNRSTYCGHGNATESLGKGYPDGCGYEQLFVSPVFTLVISLL 60
   :||| ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2 VNST-HRGMHTSLHLWNRSSYRLHNSASESLGKGYSDGGCYEQLFVSPVFTLVISLL 60

QY 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDMDAQSFTVN 120

QY 121 IDNVDSVICSSLLASICSLLSIAVDRTFTFYALQYHNIMTVRRVGIISCIWAACVTS 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 IDNVDSVICSSLLASICSLLSIAVDRTFTFYALQYHNIMTVRRVGIISCIWAACVTS 180

QY 181 GILFIYSDSTAVIICLTMTFMTLMALMASLYVHMFMLMARLHRIKRIAVLPGTGTROGAN 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 GILFIYSDSTAVIICLTMTFMTLMALMASLYVHMFMLMARLHRIKRIAVLPGTGTROGAN 240

QY 241 MKGATLTILIGVFWVWAPFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 MKGATLTILIGVFWVWAPFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300

QY 301 IYALRSQELRKTFRKIIICYPPLGGCLDLSRY 332
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 IYALRSQELRKTFRKIIICYPPLGGCLDLSRY 332

Query Match          94.2%; Score 1626.5; DB 4; Length 332;
Best Local Similarity 94.9%; Pred. No. 4.6e-125;
Matches 315; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 MNSTLQHCWHTSLHFWNRSTYCGHGNATESLGKGYPDGCGYEQLFVSPVFTLVISLL 60
   :||| ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2 VNST-HRGMHTSLHLWNRSSYRLHNSASESLGKGYSDGGCYEQLFVSPVFTLVISLL 60

QY 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDMDAQSFTVN 120

QY 121 IDNVDSVICSSLLASICSLLSIAVDRTFTFYALQYHNIMTVRRVGIISCIWAACVTS 180
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Db 121 IDNVDSVICSSLLASICSLLSIAVDRTFTFYALQYHNIMTVRRVGIISCIWAACVTS 180

QY 181 GILFIYSDSTAVIICLTMTFMTLMALMASLYVHMFMLMARLHRIKRIAVLPGTGTROGAN 240
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Db 181 GILFIYSDSTAVIICLTMTFMTLMALMASLYVHMFMLMARLHRIKRIAVLPGTGTROGAN 240

QY 241 MKGATLTILIGVFWVWAPFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
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Db 241 MKGATLTILIGVFWVWAPFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300

QY 301 IYALRSQELRKTFRKIIICYPPLGGCLDLSRY 332
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Db 301 IYALRSQELRKTFRKIIICYPPLGGCLDLSRY 332

RESULT 14
US-08-870-511-12
; Sequence 12, Application US/08870511
; Patent No. 6287763
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank
; APPLICANT: Huszar, Dennis
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE
; TITLE OF INVENTION: REGULATION OF BODY WEIGHT
; FILE REFERENCE: 7853-083
; CURRENT APPLICATION NUMBER: US/08/870,511
; CURRENT FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-870-511-12

Query Match          94.2%; Score 1626.5; DB 4; Length 332;
Best Local Similarity 94.9%; Pred. No. 4.6e-125;
Matches 315; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 MNSTLQHCWHTSLHFWNRSTYCGHGNATESLGKGYPDGCGYEQLFVSPVFTLVISLL 60
   :||| ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2 VNST-HRGMHTSLHLWNRSSYRLHNSASESLGKGYSDGGCYEQLFVSPVFTLVISLL 60

QY 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
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Db 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDMDAQSFTVN 120

QY 121 IDNVDSVICSSLLASICSLLSIAVDRTFTFYALQYHNIMTVRRVGIISCIWAACVTS 180
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Db 121 IDNVDSVICSSLLASICSLLSIAVDRTFTFYALQYHNIMTVRRVGIISCIWAACVTS 180

QY 181 GILFIYSDSTAVIICLTMTFMTLMALMASLYVHMFMLMARLHRIKRIAVLPGTGTROGAN 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 GILFIYSDSTAVIICLTMTFMTLMALMASLYVHMFMLMARLHRIKRIAVLPGTGTROGAN 240

QY 241 MKGATLTILIGVFWVWAPFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
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Db 241 MKGATLTILIGVFWVWAPFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300

QY 301 IYALRSQELRKTFRKIIICYPPLGGCLDLSRY 332
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Db 301 IYALRSQELRKTFRKIIICYPPLGGCLDLSRY 332
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Db 2 VNST-HRGMHTSLHLWNRSSYRLHNSASESLGKGYSDGGCYEQLFVSPVFTLVISLL 60
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Db 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDMDAQSFTVN 120
QY 121 IDNVDSVICSSLLASICSLLSIAVDRTFTFYALQYHNIMTVRRVGIISCIWAACVTS 180
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Db 121 IDNVDSVICSSLLASICSLLSIAVDRTFTFYALQYHNIMTVRRVGIISCIWAACVTS 180
QY 181 GILFIYSDSTAVIICLTMTFMTLMALMASLYVHMFMLMARLHRIKRIAVLPGTGTROGAN 240
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Db 181 GILFIYSDSTAVIICLTMTFMTLMALMASLYVHMFMLMARLHRIKRIAVLPGTGTROGAN 240
QY 241 MKGATLTILIGVFWVWAPFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
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Db 241 MKGATLTILIGVFWVWAPFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
QY 301 IYALRSQELRKTFRKIIICYPPLGGCLDLSRY 332
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Db 301 IYALRSQELRKTFRKIIICYPPLGGCLDLSRY 332

RESULT 15
US-09-384-302A-6
; Sequence 6, Application US/09384302A
; Patent No. 6451543
; GENERAL INFORMATION:
; APPLICANT: Kochendoerfer, Gerd G
; APPLICANT: Hunter, Christie L
; APPLICANT: Kent, Stephen B.H.
; APPLICANT: Botti, Paolo
; APPLICANT: Gryphon Sciences
; TITLE OF INVENTION: Lipid Matrix-Assisted Chemical Ligation and Synthesis
; TITLE OF INVENTION: of Membrane Polypeptides
; FILE REFERENCE: grfn-028/02WO
; CURRENT APPLICATION NUMBER: US/09/384,302A
; CURRENT FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: 09/144,964
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 09/263,971
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-384-302A-6

Query Match          93.6%; Score 1615.5; DB 4; Length 332;
Best Local Similarity 94.6%; Pred. No. 3.6e-124;
Matches 314; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

QY 1 MNSTLQHCWHTSLHFWNRSTYCGHGNATESLGKGYPDGCGYEQLFVSPVFTLVISLL 60
   :||| ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2 VNST-HRGMHTSLHLWNRSSYRLHNSASESLGKGYIEGRCYEQLFVSPVFTLVISLL 60

QY 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDMDAQSFTVN 120

QY 121 IDNVDSVICSSLLASICSLLSIAVDRTFTFYALQYHNIMTVRRVGIISCIWAACVTS 180
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Db 121 IDNVDSVICSSLLASICSLLSIAVDRTFTFYALQYHNIMTVRRVGIISCIWAACVTS 180

QY 181 GILFIYSDSTAVIICLTMTFMTLMALMASLYVHMFMLMARLHRIKRIAVLPGTGTROGAN 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 GILFIYSDSTAVIICLTMTFMTLMALMASLYVHMFMLMARLHRIKRIAVLPGTGTROGAN 240

QY 241 MKGATLTILIGVFWVWAPFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
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Db 241 MKGAIITLILIGVEVWCWAPFFLHIFYISCPQNPYCVCFMSHENLYLILMCNSIIDPL 300
Qy 301 IYALRSQELRKTKEIICCYPLGGLCDLSSRY 332
Db 301 IYALRSQELRKTKEIICCYPLGGLCDLSSRY 332

Search completed: June 4, 2003, 18:03:57
Job time : 14 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 14, 2003, 11:47:14 ; Search time 3506 Seconds
(without alignments)
16477.202 Million cell updates/sec

Title: US-09-884-211A-2
Perfect score: 1985
Sequence: 1 ctaagaccgtggggaggcag.....gaataaaaaaaaaaaaaa 1985

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg.*
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10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
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25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vl.*
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31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rod.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
1	1985	100.0	1985	6	AX342682	AX342682 Sequence	
2	1165.6	58.7	1708	6	AX342681	AX342681 Sequence	
3	1060.2	53.4	2113	4	AB021664	AB021664 Sus scrofa	
c	1012.4	51.0	161822	2	AF001645	AF001645 Homo sapi	
	1012.4	51.0	162600	9	AC091576	AC091576 Homo sapi	
c	967.4	48.7	1809	4	AF265221	AF265221 Bos taurus	
7	958.2	48.3	1671	6	AR070600	AR070600 Sequence	
8	958.2	48.3	1671	6	AR167599	AR167599 Sequence	
9	958.2	48.3	1671	9	S77415	S77415 melanocortin	
10	893.4	45.0	4783	10	AF201662	AF201662 Mus musculus	
c	11	885.6	44.6	196426	2	AC127234	AC127234 Mus musculus
	12	840.8	42.4	1640	10	RNU67863	U67863 Rattus norvegicus
13	818.8	41.2	999	9	HUMELAREC	L08603 Human melanin	
14	817.4	41.2	996	6	AR033746	AR033746 Sequence	
15	817.4	41.2	996	6	AR045086	AR045086 Sequence	
16	817.4	41.2	996	6	I81482	I81482 Sequence 7	
17	817.4	41.2	996	6	I87362	I87362 Sequence 7	
18	815.6	41.1	999	6	AR167600	AR167600 Sequence	
19	815.6	41.1	999	6	AR167601	AR167601 Sequence	
20	815.6	41.1	999	6	AR167602	AR167602 Sequence	
21	703.6	35.4	840	6	AX268311	AX268311 Sequence	
22	661.2	33.3	2224	5	AB012211	AB012211 Gallus gallus	
23	635.2	32.0	746	4	AF087937	AF087937 Sus scrofa	
24	635.2	32.0	746	6	AX268310	AX268310 Sequence	
25	541.6	27.3	669	4	AF345913	AF345913 Ovis aries	
26	518.4	26.1	969	5	AB073677	AB073677 Takifugu	
27	515.2	26.0	969	5	AB073674	AB073674 Takifugu	
28	515.2	26.0	969	5	AB073675	AB073675 Takifugu	
29	515.2	26.0	969	5	AB073676	AB073676 Takifugu	
30	515.2	26.0	969	5	AB073678	AB073678 Takifugu	
31	458.2	23.1	981	5	AY078989	AY078989 Danio rerio	
32	437.2	22.0	554	10	AB009664	AB009664 Mus musculus	
33	437.2	22.0	978	9	AF208691	AF208691 Pan troglodytes	
34	437.2	22.0	1599	10	RATM5C5R	L27081 Rat melanocortin	
35	436	22.0	1650	9	HSU08353	225470 H.sapiens melanocortin	
36	435.6	21.9	1050	9	HSU08353	U08353 Human melanin	
c	37	435.6	21.9	146096	2	AP001009	AP001009 Homo sapiens
	38	435.6	21.9	173868	2	AP001525	AP001525 Homo sapiens
c	39	435.6	21.9	183891	2	AF001086	AF001086 Homo sapiens
	40	435.2	21.9	951	5	AY078990	AY078990 Danio rerio
c	41	435.2	21.9	204185	2	AL844521	AL844521 Danio rerio
	42	432.4	21.8	1262	9	HUMMC5R	L27080 Human melanin
43	429.2	21.6	2180	10	MMGMC5R	X76295 M.musculus	
44	429.2	21.6	183619	2	AC111069	AC111069 Mus musculus	
c	45	429.2	21.6	202807	10	AC021063	AC021063 Mus Musculus

ALIGNMENTS

RESULT 1
AX342682
LOCUS AX342682
DEFINITION Sequence 2 from Patent EP1167386.
ACCESSION AX342682
VERSION AX342682.1 GI:18152062
KEYWORDS dog.
SOURCE Canis familiaris
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1
REFERENCE
AUTHORS Hickman, M.A., Houseknecht, K.L. and Robertson, A.S.
TITLE Canine and feline melanocortin-4 receptor sequences and screening assays to identify compounds useful in regulating animal appetite

AX342682 1985 bp DNA linear PAT 12-JAN-2002
Sequence 2 from Patent EP1167386.
AX342682 GI:18152062

JOURNAL		and metabolic rate	
Patent: EP 1167386-A 2 02-JAN-2002;		Patent: EP 1167386-A 2 02-JAN-2002;	
Pfizer Products Inc. (US)		Pfizer Products Inc. (US)	
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121226	contig of	27508	bp in length
139017	contig of	17691	bp in length
150492	contig of	11375	bp in length
158977	contig of	8385	bp in length
161822	contig of	2745	bp in length.

* NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* 1 56165: contig of 56165 bp in length
* 56166 56265: gap of 100 bp
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* 95519 121226: contig of 25708 bp in length
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AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 18, clone RP11-711110
2 (bases 1 to 162600)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
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Camarata,J., Campopiano,A., Chang,J., Choepel,Y., Colangelo,M.,
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Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D.,
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Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
Maclean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M.,
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Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission

TITLE
JOURNAL
REFERENCE
AUTHORS

Submitted (07-MAY-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 162600)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
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Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
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Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission

TITLE
JOURNAL
REFERENCE
AUTHORS

Submitted (14-APR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 162600)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
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Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission

TITLE
JOURNAL
REFERENCE
AUTHORS

Submitted (24-APR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
5 (bases 1 to 162600)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
Cooke,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G.,
Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,
Mihoa,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission

Submitted (25-APR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 14, 2002 this sequence version replaced gi:20128089.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L12567
Center clone name: 711_I_10

----- Location/Qualifiers
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Query Match 51.0%; Score 1012.4; DB 9; Length 162600;
Best Local Similarity 76.2%; Pred. No. 6.8e-216;
Matches 1520; Conservative 0; Mismatches 391; Indels 83; Gaps 19;

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LOCUS Bos taurus melanocortin 4 receptor (MC4R) mRNA, complete cds.
DEFINITION
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VERSION AF265221.1 GI:10443910
KEYWORDS
SOURCE Bos taurus.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 1809)
AUTHORS Haegeman,A., Coopman,F., Jacobs,K., Mattheeuws,M., Van Zeveren,A.
and Peelman,L.
TITLE Bovine melanocortin receptor 4: cDNA sequence, polymorphisms and
mapping
JOURNAL Anim. Genet. 32 (4), 189-192 (2001)
MEDLINE 21422894
PUBMED 11531696
REFERENCE 2 (bases 1 to 1809)
AUTHORS Peelman,L.J.
TITLE Direct Submission
JOURNAL Submitted (09-MAY-2000) Animal Genetics, Ghent University,
Heidestraat 19, Merelbeke 9820, Belgium
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Matches 1325; Conservative 0; Mismatches 376; Indels 32; Gaps 10;
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AF201662			AF201662.1
KEYWORDS			GI:11493678
SOURCE			Mus musculus.
ORGANISM			Mus musculus
REFERENCE			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 4783)
AUTHORS			Dumont,L.M., Wu,C.S., Aschkenasi,C.J., Elmquist,J.K., Lowell,B.B. and Mountjoy,K.G.
TITLE			Mouse melanocortin-4 receptor gene 5'-flanking region imparts cell specific expression in vitro

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QY 1698 TAGAAAAAGAAAA 1710

Db 2779 CATGAAGAAGAAAA 2791

RESULT 11
AC127234/c

LOCUS AC127234 196426 bp DNA linear HTG 17-JUL-2002
DEFINITION Mus musculus chromosome UNK clone RP24-566K14, WORKING DRAFT
ACCESSION AC127234
VERSION AC127234.1 GI:21747647
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 196426)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE The sequence of Mus musculus clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 196426)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (14-JUL-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 3 (bases 1 to 196426)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (17-JUL-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@wustl.wustl.edu
----- Project Information -----
Center project name: M_BB0566K14
----- Summary Statistics -----
Sequencing vector: M13; 0%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 192945 bases at least Q40
Consensus quality: 194032 bases at least Q30
Consensus quality: 194786 bases at least Q20

* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1101: contig of 1101 bp in length
* 1102 1201: gap of unknown length
* 1202 21995: contig of 20794 bp in length
* 21996 22095: gap of unknown length
* 22096 71743: contig of 49648 bp in length
* 71744 71843: gap of unknown length
* 71844 125305: contig of 53462 bp in length
* 125306 125405: gap of unknown length
* 125406 196426: contig of 71021 bp in length.
FEATURES
Location/Qualifiers
1..196426
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/chromosome="UNK"
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1202..21995
/note="assembly_name:Contig3"
22096..71743
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71844..125305
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misc_feature
misc_feature
misc_feature


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RESULT 12
RNU67863
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Rattus norvegicus.
Rattus norvegicus
Rattus norvegicus melanocortin-4 receptor mRNA, complete cds.
U67863
U67863.1 GI:1565664
Rattus norvegicus
Rattus norvegicus melanocortin-4 receptor mRNA, complete cds.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 1640)
Alvaro,J.D., Tatro,J.B., Quillian,J.M., Fogliano,M., Eisenhard,M.,
Lerner,M.R., Nestler,E.J. and Duman,R.S.
Morphine down-regulates melanocortin-4 receptor expression in brain
regions that mediate opiate addiction
Mol. Pharmacol. 50 (3), 583-591 (1996)
96387362
PUBMED
8794897
2 (bases 1 to 1640)
Alvaro,J.D., Duman,R.S., Fogliano,M. and Eisenhard,M.
Direct Submission
Submitted (22-AUG-1996) Psychiatry, Yale University, 34 Park St,
New Haven, CT 06508, USA
Location/Qualifiers
1..1640
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/strain="Sprague-Dawley"
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source
CDS

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/note="melanocortin receptor subtype"

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MTVRVGIIISCIWAACVTSGLFIYSDSSAVIICLITMFWMLVMSLYVHMFILM
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BASE COUNT 378 a 404 c 384 g 474 t

ORIGIN

Query Match 42.4%; Score 840.8; DB 10; Length 1640;

Best local similarity 80.1%; Pred. No. 1.1e-177;

Matches 1051; Conservative 0; Mismatches 252; Indels 9; Gaps 5;

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QY 498 CGCAGCACCTACCGAGACGACGCGCAACGACCTAGTCCCTTGGCAAAGGCTACCCCGAC 557
DB 199 CGCAGCACCGCGGTGCAGCGCAATGCCAGGAGTCTCTGGGAGGGGCACTCAGAC 258
QY 558 GGGGGATGCTACGAGCAACTCTTCGTCTCCCGGAGGTGTTCGTGACTCTGGGGGCATA 617
DB 259 GGAGGATGCTATCAGCAACTTTTGTCTCCCGGAGGTGTTTGTGACTCTGGGTGCATA 318
QY 618 AGCTTGCTGGAGAACATTCGTGTGATCGTGGGCAATAGCCNAGAACAGAAATCTGCACCTCA 677
DB 319 AGCCTTGTGGAGAACATTCGTGTGATCGTGGGCAATAGCCNAGAACAGAACTGCACCTCA 378
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DB 559 TGCAGCGCTGCTCTCAATTCGAGTGGACAGGTACTTTACTATCTTTTATGCGCTCCAGTAC 618
QY 918 CATAACATCATGACGCTGAGCGGGTGGGATCATCATCATCATCATCATCATCATCATCATCAT 977
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QY 1637 CATGCTACTTTTGGGCTGTGCATTTGTAATTCATTTCGACGCTGTAGACACTTTGAATTT 1696
DB 1333 CTGACTTTTGTGTAACAGTCTTATTTATGTTCTACAGCGTGGCGCTATGGAGTT 1392
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RESULT 13

HUMEL4REC

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

FEATURES

source

CDS

Location/Qualifiers

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BASE COUNT 229 a 243 c 213 g 314 t

ORIGIN

Query Match

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Best Local Similarity 89.2%; Pred. No. 8.4e-173; Matches 883; Conservative 0; Mismatches 107; Indels 0; Gaps 0;									
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QY	515	GCAGGGCAACGCCACTGAGTCCCTTGGCAAGGCTACCCCGCAGGGGATGCTACGAGCA	574						
Db	69	GCACAGCAATGCCAGTGAGTCCCTTGGAAAGGCTACTCTGATGGAGGGTCTACGAGCA	128						
QY	575	ACTCTTGCTCCCGGAGGTGTCGACTCTGGGGTCTAAGCTTGTCTGGAGAACAT	634						
Db	129	ACTTTTGTCTCTCTGAGGTGTTGTGACTCTGGGTGTCATCAGCTTGTGGAGAAAT	188						
QY	635	TCTGCTGATCGTGCATATAGCAAGAACTTCTGCACCTACCCATCGCTTTCAT	694						
Db	189	CTTAGTGATCTGCAATAGCAAGAACTTCTGCACCTACCCATCGCTTTCAT	248						
QY	695	CTGTAGCCTTGCCGTGGCCGATATGCTGGTGAGGGTTTCCAAACGGGTGAGAGACCAT	754						
Db	249	CTGAGCTTGCCGTGGGTGATGCTGGTGAGGGTTTCAAATGATGAGAGACCAT	308						
QY	755	CATCACCCTGTGTAACAGTACGGATACGGACGCGAGAGTTTTCACGGTGAATATGATAA	814						
Db	309	CATCACCCTATTAACAGTACAGATACGGATGACAGAGTTTTCACAGTGAATATGATAA	368						
QY	815	TGTCATTGACTCGGTGATCTGTAGCTCTGCTCGCCTCGATTTGACGCCCTGCTCTCAAT	874						
Db	369	TGTCATTGACTCGGTGATCTGTAGCTCTGCTCGCCTCGATTTGACGCCCTGCTCTCAAT	428						
QY	875	TGCAGTGGACAGGTACTTACTATCTTTATGCCCCTCCAGTACCATACATCATGACAGT	934						
Db	429	TGCAGTGGACAGGTACTTACTATCTTTTATGCCCCTCCAGTACCATACATCATGACAGT	488						
QY	935	GAGCGGGTTGGGATCATCATCAGTTGATCTGGCGGGCTTGCACGGTGTGACGGCATCTT	994						
Db	489	TAAGCGGGTTGGGATCATCATCAGTTGATCTGGCGGGCTTGCACGGTGTGACGGCATCTT	548						
QY	995	GTTTCATTGTTACTCGGACAGTACTGCTGTGTCATCATCTGCCTCATACCATGTTTTCAC	1054						
Db	549	GTTTCATTGTTACTCGGACAGTACTGCTGTGTCATCATCTGCCTCATACCATGTTTTCAC	608						
QY	1055	CATGCTGGCCCTCATGGCTTCTCTAGCTCCACATGTTTCTCATGCGCCAGCAGTACAGAT	1114						
Db	609	CATGCTGGCCCTCATGGCTTCTCTAGCTCCACATGTTTCTCATGCGCCAGCAGTACAGAT	668						
QY	1115	CAAGAGAATCCCGCTCTCCCGGCACCGCACCATCGCCAAAGGGGCAACATGAAGGG	1174						
Db	669	TAAGAGGATGCTGTCTCTCCCGGCACCTGGTGCCATCCGCCAAGGTGCCAATATGAAGGG	728						
QY	1175	TGCCATTACCTTGACCATACTCATTTGGGGTCTTGGTCTGCTGCTGCTGCTTCTCT	1234						
QY	1235	CCACTTGATATTCATATCTCTTGTCCCGAATCCATCTGCTGTGCTTCTGCTCTCA	1294						
Db	789	CCACTTAATATTCATATCTCTTGTCTCAGAATCCATATGCTGTGCTTCTGCTCTCA	848						
QY	1295	CTTTAACTTGTTACTCATCTGATCATGTGTAACATCATCATGACCCCTCATTTATGC	1354						
Db	849	CTTTAACTTGTTACTCATCTGATCATGTGTAATTCATATCATCATGCTCTGATTTATGC	908						
QY	1355	ACTCCGAGCAAGAGCTGAGGAACCTTCAAGAGATCATCTGTTGCTATCTCTCGGG	1414						
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RESULT 15
AR045086
LOCUS AR045086 996 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 7 from patent US 5817787.
ACCESSION AR045086
VERSION AR045086.1 GI:5966551
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 996)
AUTHORS Yamada,T. and Gantz,I.
TITLE Probes and methods for detecting melanocortin-5 receptor
JOURNAL Patent: US 5817787-A 7 06-OCT-1998;
FEATURES Location/Qualifiers
source 1..996
BASE COUNT 227 a 243 c 213 g 313 t
ORIGIN

Query Match 41.2%; Score 817.4; DB 6; Length 996;
Best Local Similarity 89.3%; Pred. No. 1.7e-172;
Matches 881; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

Qy 455 CACCCTTCAGCAGCGAATGACACTTCTCTCCACTTCTGGAACCGCAGCACCCTACGGACA 514
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Qy 515 GCACGGCAAGCCGACTGAGTCCCTTGGCAAGGCTACCCCGAGCGGGGATGCTACGAGCA 574
Db 69 GCACGCAATGCCAGTGAGTCCCTTGGAAAGGCTACTCTGATGGAGGGTGTCTACGAGCA 128
Qy 575 ACTCTTCGTCTCCCGGAGGTGTCTGACTCTGGGGTCAATAAGCTTGTCTGGAGAACAT 634
Db 129 ACTTTTGTCTCTCTCTGAGGTGTGTGACTCTGGGTGTCATCAGCTTGTGGAGATAT 188
Qy 635 TCTGGTGATCGTGGCAATAGCCCAAGAAATCTGCATCACCCTACTCTCTCTCTCAT 694
Db 189 CTTAGTGATTTGGCAATAGCCCAAGAAATCTGCATTCACCCCTACTCTCTCTCAT 248
Qy 695 CTGTAGCCTTGGCTGTGGCCGATATGCTGTGAGCGTTTCCACGGGTCTAGAACCATCGT 754
Db 249 CTGACGCTTGGCTGTGGCTGATGCTGTGAGCGTTTCAAAATGGATGAGAACCATTTAT 308
Qy 755 CATCACCTCTTTGAACAGTACGAGTACGGACGCGAGGTTTCAAGGTTCAATGATTAATAA 814
Db 309 CATCACCTCTTTAAACAGTACAGATACGAGTACGAGATTTCAACAGTGAATATGATAA 368
Qy 815 TGTCAATGACTCGGTGATCTGAGTCTCTGTGGCTCGATTTGACGCTCTCTCTCAAT 874
Db 369 TGTCAATGACTCGGTGATCTGAGTCTCTGTGGCTCGATTTGACGCTCTCTCTCAAT 428
Qy 875 TGCAGTGGACAGTACTTTACTATCTTTTATGCCCTCCAGTACCATAACATCATGACGT 934
Db 934 TTTTATGCCCTCCAGTACCATAACATCATGACGT 934
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Search completed: June 14, 2003, 13:03:14
Job time : 4230 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 4, 2003, 18:03:01 ; Search time 31 Seconds
(without alignments)
1105.670 Million cell updates/sec

Title: US-09-884-211A-4
Perfect score: 1726
Sequence: 1 MNSTLQHGHTSLHFWNRST.....FKETICCYPLGLCLDLSRY 332

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep.*
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- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1685	97.6	332	9	US-09-884-211A-3
3	1590	92.1	332	9	US-09-910-180-2
4	1003.5	58.1	325	12	US-10-052-545-16
5	994	57.6	323	10	US-09-903-395-2
6	752.5	43.6	317	12	US-10-052-545-2
7	723	41.9	297	9	US-10-151-431-4
8	721	41.8	296	12	US-10-015-948-2
9	700	40.6	297	9	US-10-151-431-6
10	358.5	20.8	364	9	US-09-971-228-6
11	358.5	20.8	364	9	US-09-811-838-2
12	358.5	20.8	364	10	US-09-842-316-3
13	358.5	20.8	364	10	US-09-731-030A-15
14	358.5	20.8	364	12	US-10-037-616-20
15	332	19.2	102	12	US-10-052-545-8
16	326	18.9	304	12	US-10-052-545-10
17	325.5	18.9	382	10	US-09-969-711-2
18	320.5	18.6	381	9	US-10-024-494-28
19	320.5	18.6	381	10	US-09-827-937A-18

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21	320.5	18.6	381	10	US-09-731-030A-17	Sequence 17, Appl
22	320	18.5	341	9	US-09-971-228-13	Sequence 13, Appl
23	320	18.5	346	9	US-09-971-228-15	Sequence 15, Appl
24	320	18.5	362	10	US-09-993-844-8	Sequence 8, Appli
25	320	18.5	381	12	US-10-037-616-19	Sequence 19, Appl
26	320	18.5	382	9	US-09-971-228-5	Sequence 5, Appli
27	320	18.5	382	9	US-09-759-514-2	Sequence 2, Appli
28	316.5	18.3	330	10	US-09-845-720-2	Sequence 2, Appli
29	314.5	18.2	353	9	US-09-971-228-11	Sequence 11, Appli
30	314.5	18.2	353	9	US-09-811-838-6	Sequence 6, Appli
31	314.5	18.2	353	9	US-10-097-340-338	Sequence 338, App
32	314.5	18.2	353	10	US-09-842-316-4	Sequence 4, Appli
33	314.5	18.2	353	10	US-09-731-030A-16	Sequence 16, Appl
34	314.5	18.2	353	12	US-10-037-616-25	Sequence 25, Appl
35	312.5	18.1	321	9	US-10-146-065-2	Sequence 2, Appli
36	305.5	17.7	348	10	US-09-903-799-2	Sequence 2, Appli
37	305.5	17.7	353	10	US-09-771-063-2	Sequence 2, Appli
38	305.5	17.7	353	10	US-09-771-063-4	Sequence 4, Appli
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40	305	17.7	352	9	US-10-084-507B-21	Sequence 21, Appl
41	304.5	17.6	124	12	US-10-052-545-12	Sequence 12, Appl
42	304.5	17.6	353	9	US-10-084-507B-22	Sequence 22, Appl
43	304.5	17.6	353	10	US-09-731-030A-19	Sequence 19, Appl
44	304.5	17.6	354	10	US-09-879-225-2	Sequence 2, Appli
45	303.5	17.6	353	9	US-10-084-507B-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-09-884-211A-4
; Sequence 4, Application US/09884211A
; Publication No. US20030032791A1
; GENERAL INFORMATION:
; APPLICANT: Alan et. al.
; TITLE OF INVENTION: NOVEL MELANOCORTIN-4 RECEPTOR SEQUENCES AND
; SCREENING ASSAYS TO IDENTIFY COMPOUNDS USEFUL
; IN REGULATING ANIMAL APPETITE AND METABOLIC RATE
; FILE REFERENCE: PC10743A
; CURRENT APPLICATION NUMBER: US/09/884,211A
; CURRENT FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 60/213,909
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Canine MC4R protein Sequence
US-09-884-211A-4

Query Match	100.0%	Score	1726;	DB	9;	Length	332;
Best Local Similarity	100.0%	Pred. No.	3.1e-149;				
Matches	332;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MNSTLQHGHTSLHFWNRSTYGQHGHNATESLGKYPDGGCYEQLFVSPVFTLGVISLL	60				
Db	1	MNSTLQHGHTSLHFWNRSTYGQHGHNATESLGKYPDGGCYEQLFVSPVFTLGVISLL	60				
Qy	61	ENILVIVAIANKNLSHPMYFFICSLAVADMVSVNSGSETIVITLLNSTDFAOSFTVN	120				
Db	61	ENILVIVAIANKNLSHPMYFFICSLAVADMVSVNSGSETIVITLLNSTDFAOSFTVN	120				
Qy	121	IDNWIDSVICSSLLASICSLLSIAVDRTYFTFYALQYHNIMTVRVGIIISCIWAACVTS	180				
Db	121	IDNWIDSVICSSLLASICSLLSIAVDRTYFTFYALQYHNIMTVRVGIIISCIWAACVTS	180				
Qy	181	GILFTIYSDSTAVIICLITMTFFMLMALMASLYVHMFMLARLHIKRIAVLPGTGTIRQGAN	240				
Db	181	GILFTIYSDSTAVIICLITMTFFMLMALMASLYVHMFMLARLHIKRIAVLPGTGTIRQGAN	240				

QY 241 MKGAILTLILGVVVCWAPFELHLIFYISCPQNPYCVCFMSHFNLYLILMCSNIIIDPL 300
|||||
Db 241 MKGAILTLILGVVVCWAPFELHLIFYISCPQNPYCVCFMSHFNLYLILMCSNIIIDPL 300
|||||
QY 301 IYALRSQELRKTKEIICCYPLGGCLDLSSRY 332
|||||
Db 301 IYALRSQELRKTKEIICCYPLGGCLDLSSRY 332
|||||

RESULT 2

US-09-884-211A-3
; Sequence 3, Application US/09884211A
; Publication No. US20030032791A1
; GENERAL INFORMATION:
; APPLICANT: Alan et. al.
; TITLE OF INVENTION: NOVEL MELANOCORTIN-4 RECEPTOR SEQUENCES AND
; SCREENING ASSAYS TO IDENTIFY COMPOUNDS USEFUL
; TITLE OF INVENTION: IN REGULATING ANIMAL APPETITE AND METABOLIC RATE
; FILE REFERENCE: PC10743A
; CURRENT APPLICATION NUMBER: US/09/884, 211A
; CURRENT FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 60/213,909
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Feline MC4R protein sequence
US-09-884-211A-3

Query Match 97.6%; Score 1685; DB 9; Length 332;
Best Local Similarity 97.6%; Pred. No. 1.6e-145;
Matches 324; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MNSTLQHGHTSLHFWNRSTYGGHGNATESLGGKGYDGGCYEQLFVSPFVTLGVISLL 60
|||||
Db 1 MNSTLQHGHTSLHFWNRSTYGGHGNATESLGGKGYDGGCYEQLFVSPFVTLGVISLL 60
|||||
QY 61 ENILVIVAIAKNKLNHSPMYFFTCISLAVADMLVSVNGSETIVITLLNSTDDAQSFVN 120
|||||
Db 61 ENILVIVAIAKNKLNHSPMYFFTCISLAVADMLVSVNGSETIVITLLNSTDDAQSFVN 120
|||||
QY 121 IDNVDSVCSSLLASICSLSLSTAVDRYFTFYALQYHNIMTVRRVGGIISCIWAACVTS 180
Db 121 IDNVDSVCSSLLASICSLSLSTAVDRYFTFYALQYHNIMTVRRVGGIISCIWAACVTS 180
|||||
QY 181 GILFIYSDSTAVIICLTIMFTMLALMASLYVHMFELMARLHKRIAVLPGTGTIRQGAN 240
Db 181 GILFIYSDSTAVIICLTIMFTMLALMASLYVHMFELMARLHKRIAVLPGTGTIRQGAN 240
|||||
QY 241 MKGAILTLILGVVVCWAPFELHLIFYISCPQNPYCVCFMSHFNLYLILMCSNIIIDPL 300
Db 241 MKGAILTLILGVVVCWAPFELHLIFYISCPQNPYCVCFMSHFNLYLILMCSNIIIDPL 300
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QY 301 IYALRSQELRKTKEIICCYPLGGCLDLSSRY 332
Db 301 IYALRSQELRKTKEIICCYPLGGCLDLSSRY 332
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RESULT 3

US-09-910-180-2
; Sequence 2, Application US/09910180
; Publication No. US20030082678A1
; GENERAL INFORMATION:
; APPLICANT: Hsiung, Hansen
; APPLICANT: Smith, Dennis
; APPLICANT: Zhang, Xing-yue
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING BODY WEIGHT IN BOVINE SPECIES
; FILE REFERENCE: P-12621
; CURRENT APPLICATION NUMBER: US/09/910,180
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Bovine
US-09-910-180-2

Query Match 92.1%; Score 1590; DB 9; Length 332;
Best Local Similarity 93.1%; Pred. No. 7.3e-137;
Matches 309; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 1 MNSTLQHGHTSLHFWNRSTYGGHGNATESLGGKGYDGGCYEQLFVSPFVTLGVISLL 60
Db 1 MNSTLQHGHTSLHFWNRSTYGGHGNATESLGGKGYDGGCYEQLFVSPFVTLGVISLL 60
|||||
QY 61 ENILVIVAIAKNKLNHSPMYFFTCISLAVADMLVSVNGSETIVITLLNSTDDAQSFVN 120
Db 61 ENILVIVAIAKNKLNHSPMYFFTCISLAVADMLVSVNGSETIVITLLNSTDDAQSFVN 120
|||||
QY 121 IDNVDSVCSSLLASICSLSLSTAVDRYFTFYALQYHNIMTVRRVGGIISCIWAACVTS 180
Db 121 IDNVDSVCSSLLASICSLSLSTAVDRYFTFYALQYHNIMTVRRVGGIISCIWAACVTS 180
|||||
QY 181 GILFIYSDSTAVIICLTIMFTMLALMASLYVHMFELMARLHKRIAVLPGTGTIRQGAN 240
Db 181 GILFIYSDSTAVIICLTIMFTMLALMASLYVHMFELMARLHKRIAVLPGTGTIRQGAN 240
|||||
QY 241 MKGAILTLILGVVVCWAPFELHLIFYISCPQNPYCVCFMSHFNLYLILMCSNIIIDPL 300
Db 241 MKGAILTLILGVVVCWAPFELHLIFYISCPQNPYCVCFMSHFNLYLILMCSNIIIDPL 300
|||||
QY 301 IYALRSQELRKTKEIICCYPLGGCLDLSSRY 332
Db 301 IYALRSQELRKTKEIICCYPLGGCLDLSSRY 332
|||||

RESULT 4

US-10-052-545-16
; Sequence 16, Application US/10052545
; Patent No. US20020142392A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Melanocyte stimulating hormone receptor
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/052,545
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/387,805
; FILING DATE: 21-FEB-95
; APPLICATION NUMBER: PCT/DK93/00273
; FILING DATE: 20-AUG-93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 1046/92
; FILING DATE: 21-AUG-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 1118/92
; FILING DATE: 10-SEP-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0528/93

Query Match	57.6%	Score 994;	DB 10;	Length 323;
Best Local Similarity	61.7%;	Pred. No. 1.2e-82;		
Matches 182;	Conservative	53;	Mismatches 52;	Indels
QY	27	ATGSLCKGYPDGGCYEQLEFSPSEVFTLGVISLENNILVIAAKNNLHLS		

Qy 262 FLHLIFYSCPQNPYCVCFMSHFNLYLILIMCNSIIDPLIYALRSQELRKTFTKEIICC 319
Db 236 VLHVLLTFCFNPYCVCFMSHFNLYLILIMCNSIIDPLIYALRSQELRKTFTKEIICC 293

RESULT 9

US-10-151-431-6
; Sequence 6, Application US/10151431
; Publication No. US20030044973A1
GENERAL INFORMATION:
; APPLICANT: Cone, Roger D
; Mountjoy, Kathleen G
; TITLE OF INVENTION: Mammalian Adrenocorticotrophic Hormone
; Receptors and Uses
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Alleghetti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/151.431
; FILING DATE: 20-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/105.298
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/866.560
; FILING DATE: 10-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20030044973A1nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 297 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-151-431-6

Query Match 40.6%; Score 700; DB 9; Length 297;
Best Local Similarity 49.6%; Pred. No. 6.2e-56;
Matches .135; Conservative 47; Mismatches 82; Indels 8; Gaps 2;

Qy 49 EVFVTLGVISLLENILVIVAIKNNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLN 108
Db 29 EIFFTVSIGVLENLWLVAVAKNLSQSPMYFFICSLAISDMLSGLYKILENVLMFKN 88
Qy 109 STDTDAO-STVTNIDNVDSVICSLLASISIAVDYFTIFYALQVHNIMTVRRVG 167
Db 89 MGYLEPGSFESTADDVDSVLISLGLSICSUSVIAADRYITIFHALQVHRIMTPAPCP 148
Qy 168 IITSICWAACVSGILFIYSDSTAVIICLITFTFTMLMASLYVHMFLMARLHIKRIA 227
Db 149 RHLTVLWAGTSGITIVTSHVPTVIALEPLMLAFILCYVHMFLMARLHSHTRTP 208
Qy 228 VLPCTGTIROGANKMGAIITILIGVFCVWAPFFLHLIFYISCPQNPYCVCFMSHFNLY 287
Db 209 SLP-----KANMRGAVTLTVLGVIFCWAPEVLHVLLMTFCPADPYCACYMSLFQVN 261

Qy 288 LILIMCNSIIDPLIYALRSQELRKTFTKEIICC 319
Db 262 GVLMCNAIDPFYAFRSPELRYAFKRWVIC 293

RESULT 10

US-09-971-228-6
; Sequence 6, Application US/09971228
; Patent No. US20020155512A1
GENERAL INFORMATION:
; APPLICANT: Liao, X. Charlene
; APPLICANT: Masuda, Esteban
; APPLICANT: Chu, Peter
; APPLICANT: Pardo, Jorge
; APPLICANT: Li, Congfen
; APPLICANT: Zhao, Haoran
; APPLICANT: Jiang, Yingping
; APPLICANT: Rigel Pharmaceuticals, Incorporated
; TITLE OF INVENTION: EDG: Modulators of Lymphocyte Activation and Migration
; FILE REFERENCE: 021044-000310US
; CURRENT APPLICATION NUMBER: US/09/971,228
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/284,763
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human endothelial differentiation G-protein
; OTHER INFORMATION: coupled receptor (GPCR) 2 (EDG2)
US-09-971-228-6

Query Match 20.8%; Score 358.5; DB 9; Length 364;
Best Local Similarity 28.4%; Pred. No. 9.3e-25;
Matches 93; Conservative 67; Mismatches 113; Indels 55; Gaps 11;

Qy 15 FWRSTYQGH----GNATESLGKGYPDGGCYEQFLVSPVFTVLGVISLLENILVIVAIA 70
Db 33 FYNRS--GKHLATEWNTVSKLVMG-----LGITVCIFMLANLLVWVAIY 75
Qy 71 KKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAOFSFVNIDNVDSVIC 130
Db 76 VNRHFHPIYYLMLANLAAADFFAGLA-----YFLMFTGNTFRLTLVSWLLRQGLID 129
Qy 131 SLLASICSLLSIAVDYFTIFYALQVHNIMTVRRVGIIISCIWAACVSGI----- 182
Db 130 TSLTASVANLLAIAERHITVF-RMQLHTRMSNRVVVVIVITMAIVMGAIPSVGNWC 188
Qy 183 -----LFIIYSDSTAVIICLITFTFTMLMASLYVHMFLMARLHIKRIAVLPCTG 233
Db 189 ICDIENGSNMPLYSDSYLVFWAIFNL--VTFVVMVLYAHIFGVYVQRTWRMS-RHSSG 245
Qy 234 TIROGANKMGAI-FLTILIGVFCVWAPFFLHLIFYISCPQNPYCVG-FMSHFNLYLILI 291
Db 246 PRNRDTRMSLLKTVIVLIGAFIICWTPLGLVLLLDVCCPQ-----CDVLAYERFLLLA 300
Qy 292 MCNSIIDPLIYALRSQELRKTFTKEIICC 319
Db 301 EFNSAMNPIIYSDKEMSATFROIICC 328

RESULT 11

US-09-811-838-2
; Sequence 2, Application US/09811838
; Publication No. US20030027800A1
GENERAL INFORMATION:
; APPLICANT: Miller, Duane D.
; APPLICANT: Tigyi, Gabor
; APPLICANT: Dalton, James T.

Db 189 ICDIENCSNAPLYSDSYLVFWAIFNL--VTFVVMVLYAHIFGYVRQTRMS-RHSSG 245
Qy 234 TIROGANMKGAI-TLTILIGVVCWAPFFLHLIFYSQPNPCVC-FMSHFNLYLILI 291
Db 246 PRRNRTMMSLUKTVIVGLAFICWTPGLVLLLDVCCPO-----CDVLAYERFELLLA 300
Qy 292 MCNSIIDPLIYALRSQELRTFKETIIC 319
Db 301 EFNSAMNPIIYSYRDKEMSAFTRQILCC 328

RESULT 14

US-10-037-616-20
; Sequence 20, Application US/10037616
; Patent No. US20020123148A1
; GENERAL INFORMATION:
; APPLICANT: English, Denis
; APPLICANT: Kovacs, Richard J.
; APPLICANT: Rizzo, Maria T.
; APPLICANT: Sliva, Daniel T.
; TITLE OF INVENTION: Sphingolipid Compositions and Methods for Their Therapeutic Use
; FILE REFERENCE: 7042-119
; CURRENT APPLICATION NUMBER: US/10/037,616
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/243,887
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-037-616-20

Query Match 20.8%; Score 358.5; DB 12; Length 364;
Best Local Similarity 28.4%; Pred. No. 9.3e-25;
Matches 93; Conservative 67; Mismatches 113; Indels 55; Gaps 11;
Qy 15 FWNSTYGOH---GNATESIGKGYPDGCGVEQLFVSPVEVTLGVISLLENILVIVAIA 70
Db 33 FYNRS--GKHLATWNTVSKLVMG-----LGITVCIFIMLANLLVMVAIY 75
Qy 71 KKNLHSPMPYFFICSLAVADMLVSVNGSETIVITLLNSTDTDAQSFTVNTDNDVDSVIC 130
Db 76 VNRFRFPYIYLMANLAADFFAGIA-----YFLMPTGPNTRRLTVSTWLLRQGLID 129
Qy 131 SSLASICSLSIADRYFTIFYALQYHNIMTVRRVGGIISCIWAACVTSGI----- 182
Db 130 TSLTASVANLLAIAERHITVF-RMQLHTRMSNRVVVIVVWMTAIVMGAIFSVGWN 188
Qy 183 -----LEFIYSDSTAVICITMTFFMLMASLYVHMFLMARLHKRIAVLPOTG 233
Db 189 ICDIENCSNAPLYSDSYLVFWAIFNL--VTFVVMVLYAHIFGYVRQTRMS-RHSSG 245
Qy 234 TIROGANMKGAI-TLTILIGVVCWAPFFLHLIFYSQPNPCVC-FMSHFNLYLILI 291
Db 246 PRRNRTMMSLUKTVIVGLAFICWTPGLVLLLDVCCPO-----CDVLAYERFELLLA 300
Qy 292 MCNSIIDPLIYALRSQELRTFKETIIC 319
Db 301 EFNSAMNPIIYSYRDKEMSAFTRQILCC 328

RESULT 15

US-10-052-545-8
; Sequence 8, Application US/10052545
; Patent No. US20020142392A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Melanocyte stimulating hormone receptor
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/052,545
; FILING DATE:

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/387,805
; FILING DATE: 21-FEB-95
; APPLICATION NUMBER: PCT/DK93/00273
; FILING DATE: 20-AUG-93

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 1046/92
; FILING DATE: 21-AUG-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 1118/92
; FILING DATE: 10-SEP-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0528/93
; FILING DATE: 05-MAY-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 1102.0160000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
US-10-052-545-8

Query Match 19.2%; Score 332; DB 12; Length 102;
Best Local Similarity 60.8%; Pred. No. 5.3e-23;
Matches 62; Conservative 19; Mismatches 21; Indels 0; Gaps 0;

Qy 152 FYALQYHNIMTVRRVGGIISCIWAACVTSGILFIYSDSTAVICITMTFFMLMASL 211
Db 1 FYALRYHSIVTARRSGAIIAGIWAFCCTCGGIVFIYSESTYVILCLISNFFAMFLIVSL 60
Qy 212 YVHFMFLMARLHKRIAVLPGGTTRQGANMKGAITLTILIGV 253
Db 61 YIHMFLARTHVKRIALCPGPAIRGPGACRGAVTTLILGI 102

Search completed: June 4, 2003, 18:13:54
Job time : 32 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 4, 2003, 17:58:46 ; Search time 220.5 Seconds
(without alignments)
970.755 Million cell updates/sec

Title: US-09-884-211A-4

Perfect score: 1726

Sequence: 1 MNSTLQHGHTSLHFWNRST.....FKETICCPGLGLDLSRY 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US081_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US082_COMB.pep.*
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21: /cgn2_6/ptodata/1/paa/US097_COMB.pep.*
22: /cgn2_6/ptodata/1/paa/US098_COMB.pep.*
23: /cgn2_6/ptodata/1/paa/US099_COMB.pep.*
24: /cgn2_6/ptodata/1/paa/US100_COMB.pep.*
25: /cgn2_6/ptodata/1/paa/US101_COMB.pep.*
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27: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1726	100.0	332	22	US-09-884-211A-4
2	1685	97.6	332	22	US-09-884-211A-3
3	1639.5	95.0	332	27	US-60-212-655-684
4	1638.5	94.9	332	6	US-08-200-711-8
5	1638.5	94.9	332	6	US-08-200-711B-8
6	1638.5	94.9	332	10	US-08-671-525A-8

7	1638.5	94.9	332	10	US-08-672-109A-8	Sequence 8, Appli
8	1638.5	94.9	332	11	US-08-780-749-2	Sequence 2, Appli
9	1638.5	94.9	332	15	US-09-144-964-9	Sequence 9, Appli
10	1638.5	94.9	332	16	US-09-263-971-9	Sequence 9, Appli
11	1638.5	94.9	332	25	US-10-129-897-2	Sequence 2, Appli
12	1638.5	94.9	332	26	US-10-207-330-9	Sequence 2, Appli
13	1632.5	94.6	332	1	PCT-US01-11943-3	Sequence 3, Appli
14	1632.5	94.6	332	11	US-08-780-749-6	Sequence 6, Appli
15	1632.5	94.6	332	17	US-09-322-695-2	Sequence 2, Appli
16	1632.5	94.6	332	17	US-09-368-216-2	Sequence 2, Appli
17	1632.5	94.6	332	17	US-09-368-216-2	Sequence 2, Appli
18	1632.5	94.6	332	17	US-09-385-763-4	Sequence 4, Appli
19	1632.5	94.6	332	18	US-09-416-760-74	Sequence 74, Appli
20	1632.5	94.6	332	22	US-09-416-760A-74	Sequence 74, Appli
21	1632.5	94.6	332	22	US-09-876-252-74	Sequence 4, Appli
22	1632.5	94.6	332	23	US-09-981-698-4	Sequence 4, Appli
23	1632.5	94.6	332	23	US-09-981-698A-4	Sequence 4, Appli
24	1632.5	94.6	332	26	US-10-226-594-4	Sequence 4, Appli
25	1627.5	94.3	332	18	US-09-416-760-136	Sequence 136, App
26	1627.5	94.3	332	18	US-09-416-760A-136	Sequence 136, App
27	1627.5	94.3	332	22	US-09-876-252-136	Sequence 136, App
28	1624.5	94.1	332	1	PCT-US99-25767-2	Sequence 2, Appli
29	1624.5	94.1	332	15	US-09-144-964-6	Sequence 6, Appli
30	1624.5	94.1	332	22	US-09-831-206-2	Sequence 2, Appli
31	1620.5	93.9	332	17	US-09-322-695-6	Sequence 6, Appli
32	1620.5	93.9	332	17	US-09-368-216-6	Sequence 6, Appli
33	1615.5	93.6	332	16	US-09-263-971-6	Sequence 6, Appli
34	1615.5	93.6	332	26	US-10-207-330-6	Sequence 6, Appli
35	1592.5	92.3	332	17	US-09-353-099-16	Sequence 16, Appli
36	1592.5	92.3	332	24	US-10-074-754-2	Sequence 2, Appli
37	1590	92.1	332	23	US-09-910-180-2	Sequence 2, Appli
38	1490	86.3	293	15	US-09-144-964-8	Sequence 8, Appli
39	1463	84.8	311	17	US-09-380-419A-3	Sequence 3, Appli
40	1463	84.8	311	19	US-09-538-165A-3	Sequence 3, Appli
41	1463	84.8	311	19	US-09-538-165B-3	Sequence 3, Appli
42	1405	81.4	293	16	US-09-263-971-8	Sequence 8, Appli
43	1405	81.4	293	26	US-10-207-330-8	Sequence 8, Appli
44	1257	72.8	248	17	US-09-380-419A-4	Sequence 4, Appli
45	1257	72.8	248	19	US-09-538-165A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-884-211A-4
; Sequence 4, Application US/09884211A
; GENERAL INFORMATION:
; APPLICANT: Alan et, al.
; TITLE OF INVENTION: NOVEL MELANOCORTIN-4 RECEPTOR SEQUENCES AND SCREENING ASSAYS TO IDENTIFY COMPOUNDS USEFUL IN REGULATING ANIMAL APPETITE AND METABOLIC RATE
; TITLE OF INVENTION: IN REGULATING ANIMAL APPETITE AND METABOLIC RATE
; FILE REFERENCE: PCT/0743A
; CURRENT APPLICATION NUMBER: US/09/884.211A
; CURRENT FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 60/213,909
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Canine MC4R protein Sequence
US-09-884-211A-4

Query Match 100.0%; Score 1726; DB 22; Length 332;
Best Local Similarity 100.0%; Pred. No. 2.5e-151;
Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MNSTLQHGHTSLHFWNRSTYQHGHNATESLGKYPDGGCYQLFVSPVFTLGVISLL 60
Db 1 MNSTLQHGHTSLHFWNRSTYQHGHNATESLGKYPDGGCYQLFVSPVFTLGVISLL 60

QY 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMVSVNGSETIVITLLNSTDTDAQSFTVN 120
Db 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMVSVNGSETIVITLLNSTDTDAQSFTVN 120
QY 121 IDNVDSVICSLLASICSLLSIAVDRTFTFYALQYHNMVRRVGGIIISCIWAACVTS 180
Db 121 IDNVDSVICSLLASICSLLSIAVDRTFTFYALQYHNMVRRVGGIIISCIWAACVTS 180
QY 181 GILFIIYSDSTAVIICLTMTFMTLMALMASLVHMFMLARLHKRIAVLPGTGTIROGAN 240
Db 181 GILFIIYSDSTAVIICLTMTFMTLMALMASLVHMFMLARLHKRIAVLPGTGTIROGAN 240
QY 241 MKGAILTLILIGVVFVVCWAPFHLFIYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
Db 241 MKGAILTLILIGVVFVVCWAPFHLFIYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
QY 301 IVALRSQELRKTFKEIICCPYLGGLCLSSRY 332
Db 301 IVALRSQELRKTFKEIICCPYLGGLCLSSRY 332

RESULT 2

US-09-884-211A-3
; Sequence 3, Application US/09884211A
; GENERAL INFORMATION:
; APPLICANT: Alan et, al.
; TITLE OF INVENTION: NOVEL MELANOCORTIN-4 RECEPTOR SEQUENCES AND
; TITLE OF INVENTION: SCREENING ASSAYS TO IDENTIFY COMPOUNDS USEFUL
; TITLE OF INVENTION: IN REGULATING ANIMAL APPETITE AND METABOLIC RATE
; FILE REFERENCE: PC10743A
; CURRENT APPLICATION NUMBER: US/09/884, 211A
; CURRENT FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 60/213, 909
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Feline MC4R protein Sequence
US-09-884-211A-3

Query Match 97.6%; Score 1685; DB 22; Length 332;
Best Local Similarity 97.6%; Pred. No. 1.6e-147;
Matches 324; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MNSTLQHGHTSLHFWNRSTYGOHGNATESLGKGYDGGCYEQLEFVSPEVFTLGVISLL 60
Db 1 MNSTLHGHHTSLHFWNRSTYGOHGNATESLGKGYDGGCYEQLEFVSPEVFTLGVISLL 60
QY 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMVSVNGSETIVITLLNSTDTDAQSFTVN 120
Db 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMVSVNGSETIVITLLNSTDTDAQSFTVN 120
QY 121 IDNVDSVICSLLASICSLLSIAVDRTFTFYALQYHNMVRRVGGIIISCIWAACVTS 180
Db 121 IDNVDSVICSLLASICSLLSIAVDRTFTFYALQYHNMVRRVGGIIISCIWAACVTS 180
QY 181 GILFIIYSDSTAVIICLTMTFMTLMALMASLVHMFMLARLHKRIAVLPGTGTIROGAN 240
Db 181 GILFIIYSDSTAVIICLTMTFMTLMALMASLVHMFMLARLHKRIAVLPGTGTIROGAN 240
QY 241 MKGAILTLILIGVVFVVCWAPFHLFIYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
Db 241 MKGAILTLILIGVVFVVCWAPFHLFIYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
QY 301 IVALRSQELRKTFKEIICCPYLGGLCLSSRY 332
Db 301 IVALRSQELRKTFKEIICCPYLGGLCLSSRY 332

RESULT 3

US-60-212-655-684

; Sequence 684, Application US/60212655
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL0000681
; CURRENT APPLICATION NUMBER: US/60/212,655
; CURRENT FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 1131
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 684
; LENGTH: 332
; TYPE: PRT
; ORGANISM: HUMAN
US-60-212-655-684

Query Match 95.0%; Score 1639.5; DB 27; Length 332;
Best Local Similarity 95.8%; Pred. No. 2.7e-143;
Matches 318; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

QY 1 MNSTLQHGHTSLHFWNRSTYGOHGNATESLGKGYDGGCYEQLEFVSPEVFTLGVISLL 60
Db 2 VNST-HRGHTSLHFWNRSSYRLHNSASESLGKGYDGGCYEQLEFVSPEVFTLGVISLL 60
QY 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMVSVNGSETIVITLLNSTDTDAQSFTVN 120
Db 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMVSVNGSETIVITLLNSTDTDAQSFTVN 120
QY 121 IDNVDSVICSLLASICSLLSIAVDRTFTFYALQYHNMVRRVGGIIISCIWAACVTS 180
Db 121 IDNVDSVICSLLASICSLLSIAVDRTFTFYALQYHNMVRRVGGIIISCIWAACVTS 180
QY 181 GILFIIYSDSTAVIICLTMTFMTLMALMASLVHMFMLARLHKRIAVLPGTGTIROGAN 240
Db 181 GILFIIYSDSTAVIICLTMTFMTLMALMASLVHMFMLARLHKRIAVLPGTGTIROGAN 240
QY 241 MKGAILTLILIGVVFVVCWAPFHLFIYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
Db 241 MKGAILTLILIGVVFVVCWAPFHLFIYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
QY 301 IVALRSQELRKTFKEIICCPYLGGLCLSSRY 332
Db 301 IVALRSQELRKTFKEIICCPYLGGLCLSSRY 332

RESULT 4

US-08-200-711-8
; Sequence 8, Application US/08200711
; GENERAL INFORMATION:
; APPLICANT: Yamada, Tadataka
; APPLICANT: Gantz, Ira
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: US
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/200,711
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, DeAnn F. 36683
; REGISTRATION NUMBER:

Query Match 94.9%; Score 1638.5; DB 6; Length 332;
Best Local Similarity 95.5%; Pred. No. 3.4e-143;
Matches 317; Conservative 6; Mismatches 8; Indels 1;

Query Match 94.9%; Score 1638.5; DB 6; Length 332;
Best Local Similarity 95.5%; Pred. No. 3.4e-143;
Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

	Qy	1	MNSTLGHMHTSLHFWNRSTYGOHGHNATPSLGKGYDGGCYEQOLFVSPEVFTGLVISLL	60
	Dd	2	VSET::HRGMHTSLHLWNRSYRUHSNASESLGKGYSDGGCYEQOLFVSPEVFTGLVISLL	60
	Qy	61	ENILVIVAIAKNKNLSHPMYFFICSLAVADMLSVSNGSETIIVITLLNSTDTDAQSFTVN	120
	Dd	61	ENILVIVAIAKNKNLSHPMYFFICSLAVADMLSVSNGSETIIITLLNSTDTDAQSFTVN	120
	Qy	121	IDNVDSVICSSLASICSLLSTAVDRYETIFVALOYNHMTVRRYGIIISCILWAACTVS	180
	Dd	121	IDNVDSVICSSLASICSLLSTAVDRYETIFVALOYNHMTVKRGYIISCILWAACTVS	180
	Qy	181	GILFIYSDSTAVIIICLTIMFTMLMALMASLYVHMFLMARLHKRIAVLPGTGITIRQGAN	240
	Dd	181	GILFIYSDSSAVIIICLTIMFTMLMALMASLYVHMFLMARLHKRIAVLPGTGAIRQGAN	240
	Qy	241	MKGAIITLTILIGVFVVCWAPFFLHLIFYISCPNPYCVCFMSHFNLYLILMCNSIIDPL	300
	Dd	241	MKGAIITLTILIGVFVVCWAPFFLHLIFYISCPNPYCVCFMSHFNLYLILMCNSIIDPL	300
	Qy	301	IYALRSGEQLRKTEKIICCCPYLGGGLDLSSRY	332
	Dd	301	IYALRSGEQLRKTEKIICCCPYLGGGLDLSSRY	332

RESULT 6
US-08-671-525A-8
: Sequence 8. Application US/08671525A

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RESULT 6
US-08-671-525A-8
; Sequence 8, Application US/08671525A
; GENERAL INFORMATION:
; APPLICANT: Yamada, Tadataka
; APPLICANT: Gantz, Ira
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce
; STREET: P. O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: US
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/98/671-525A

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FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, DeAnn F.
REGISTRATION NUMBER: 36683
REFERENCE/DOCKET NUMBER: 2115-00853
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810)641-1600
TELEFAX: (810)641-0270
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

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Qy 1 MNSTLQGMHTSLHFWNRSTYQGHGNATESLGKGYPDGGCYEQLFVSPVFTLGVISLL 60
Db :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
2 VNST-HRGMHTSLHWNRSYRLHNSASESLGKGYSDGGCYEQLFVSPVFTLGVISLL 60
Qy 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFVN 120
Db :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFVN 120
Qy 121 IDNVDSVICSLLASICSLLSIADRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
Db :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 IDNVDSVICSLLASICSLLSIADRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
Qy 181 GILFIYSDTAVIICLITMFTMLMASLYVHMFMLARLHRIKRIAVLPCTGTIRQGAN 240
Db :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 GILFIYSDSVAIICLITMFTMLMASLYVHMFMLARLHRIKRIAVLPCTGTIRQGAN 240
Qy 241 MKGAIITLILGVVVCWAPFELHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
Db :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
241 MKGAIITLILGVVVCWAPFELHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
Qy 301 IYALRSQELRKTKEIICCYPLGGCLDSRY 332
Db :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 IYALRSQELRKTKEIICCYPLGGCLDSRY 332
```

RESULT 9

```
US-09-144-964-9
; Sequence 9, Application US/09144964
; GENERAL INFORMATION:
; APPLICANT: Kochendoerfer, Gerd G.
; APPLICANT: Hunter, Christie L.
; APPLICANT: Kent, Stephen B.H.
; APPLICANT: Botti, Paolo
; TITLE OF INVENTION: Lipid Matrix-Assisted Chemical Ligation and Synthesis
; FILE REFERENCE: GRF028/0005
; CURRENT APPLICATION NUMBER: US/09/144.964
; EARLIER FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:semi-synthetic
US-09-144-964-9
```

```
Query Match 94.9%; Score 1638.5; DB 15; Length 332;
Best Local Similarity 95.5%; Pred. No. 3.4e-143;
Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

Qy 1 MNSTLQGMHTSLHFWNRSTYQGHGNATESLGKGYPDGGCYEQLFVSPVFTLGVISLL 60
Db :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
2 VNST-HRGMHTSLHWNRSYRLHNSASESLGKGYSDGGCYEQLFVSPVFTLGVISLL 60
Qy 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFVN 120
Db :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFVN 120
Qy 121 IDNVDSVICSLLASICSLLSIADRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
Db :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 IDNVDSVICSLLASICSLLSIADRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
Qy 181 GILFIYSDTAVIICLITMFTMLMASLYVHMFMLARLHRIKRIAVLPCTGTIRQGAN 240
Db :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 GILFIYSDSVAIICLITMFTMLMASLYVHMFMLARLHRIKRIAVLPCTGTIRQGAN 240
Qy 241 MKGAIITLILGVVVCWAPFELHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
Db :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
241 MKGAIITLILGVVVCWAPFELHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
Qy 301 IYALRSQELRKTKEIICCYPLGGCLDSRY 332
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Db 301 IYALRSQELRKTKEIICCYPLGGCLDSRY 332
RESULT 10
US-09-263-971-9
; Sequence 9, Application US/09263971
; GENERAL INFORMATION:
; APPLICANT: Kochendoerfer, Gerd G.
; APPLICANT: Hunter, Christie L.
; APPLICANT: Kent, Stephen B.H.
; APPLICANT: Botti, Paolo
; TITLE OF INVENTION: Lipid Matrix-Assisted Chemical Ligation and Synthesis
; FILE REFERENCE: GRN 028/0105
; CURRENT APPLICATION NUMBER: US/09/263.971
; EARLIER FILING DATE: 1999-03-05
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
US-09-263-971-9

Query Match 94.9%; Score 1638.5; DB 16; Length 332;
Best Local Similarity 95.5%; Pred. No. 3.4e-143;
Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

Qy 1 MNSTLQGMHTSLHFWNRSTYQGHGNATESLGKGYPDGGCYEQLFVSPVFTLGVISLL 60
Db :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
2 VNST-HRGMHTSLHWNRSYRLHNSASESLGKGYSDGGCYEQLFVSPVFTLGVISLL 60
Qy 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFVN 120
Db :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFVN 120
Qy 121 IDNVDSVICSLLASICSLLSIADRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
Db :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 IDNVDSVICSLLASICSLLSIADRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
Qy 181 GILFIYSDTAVIICLITMFTMLMASLYVHMFMLARLHRIKRIAVLPCTGTIRQGAN 240
Db :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 GILFIYSDSVAIICLITMFTMLMASLYVHMFMLARLHRIKRIAVLPCTGTIRQGAN 240
Qy 241 MKGAIITLILGVVVCWAPFELHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
Db :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
241 MKGAIITLILGVVVCWAPFELHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
Qy 301 IYALRSQELRKTKEIICCYPLGGCLDSRY 332
Db :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 IYALRSQELRKTKEIICCYPLGGCLDSRY 332
```

RESULT 11

```
US-10-129-897-2
; Sequence 2, Application US/10129897
; GENERAL INFORMATION:
; APPLICANT: Van der Ploeg, Leonardus H.T.
; APPLICANT: Chen, Howard Y.
; APPLICANT: Metzger, Joseph M.
; APPLICANT: Forrest, Michael J.
; APPLICANT: MacIntyre, Duncan E.
; APPLICANT: Palyha, Oksana C.
; APPLICANT: Feighner, Scott D.
; TITLE OF INVENTION: MELANOCORTIN-4 RECEPTOR DEFICIENT CELLS,
; TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS AND METHODS OF SELECTING
; TITLE OF INVENTION: COMPOUNDS WHICH REGULATE BODY WEIGHT
```


Qy 181 GILFIYSDSTAVIICLITMFTMALMASLYVHMFMLMARLHIKRIAVLPCTGTIROGAN 240
 Db 181 GILFIYSDSTAVIICLITMFTMALMASLYVHMFMLMARLHIKRIAVLPCTGTIROGAN 240
 Qy 241 MKGAIITILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMCSIIDPL 300
 Db 241 MKGAIITILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMCSIIDPL 300
 Qy 301 IYALRSQELRKTKEIICCYPLGGCLDLSRY 332
 Db 301 IYALRSQELRKTKEIICCYPLGGCLDLSRY 332

RESULT 14
 US-08-780-749-6
 ; Sequence 6, Application US/08780749
 ; GENERAL INFORMATION:
 ; APPLICANT: Lee, Frank
 ; APPLICANT: Huszar, Dennis
 ; APPLICANT: Gu, Wei
 ; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS
 ; TITLE OF INVENTION: USEFUL IN THE REGULATION OF BODY WEIGHT
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036/2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/780,749
 ; FILING DATE: 08-JAN-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Laura A. Coruzzi
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7853-064
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-8864/9741
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 332 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-08-780-749-6

Query Match 94.6%; Score 1632.5; DB 11; Length 332;
 Best Local Similarity 95.2%; Pred. No. 1.2e-142;
 Matches 316; Conservative 6; Mismatches 9; Indels 1; Gaps 1;
 Qy 1 MNSTLQGHMTSLHFWNRSTYGOHGNATESLKGYPDGGCYEQLFVSPVEFVTLGVISLL 60
 Db 2 VNST-HRGMHTSLHLNRRSYRLHNSNASESLGKGYSDGGCYEQLFVSPVEFVTLGVISLL 60
 Qy 61 ENILVIVAIKAKNLHSPMFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFVN 120
 Db 61 ENILVIVAIKAKNLHSPMFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFVN 120
 Qy 121 IDNVDSVICSSLLASCSLSIAVDRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
 Db 121 IDNVDSVICSSLLASCSLSIAVDRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
 Qy 181 GILFIYSDSTAVIICLITMFTMALMASLYVHMFMLMARLHIKRIAVLPCTGTIROGAN 240
 Db 181 GILFIYSDSTAVIICLITMFTMALMASLYVHMFMLMARLHIKRIAVLPCTGTIROGAN 240
 Qy 241 MKGAIITILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMCSIIDPL 300
 Db 241 MKGAIITILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMCSIIDPL 300
 Qy 301 IYALRSQELRKTKEIICCYPLGGCLDLSRY 332
 Db 301 IYALRSQELRKTKEIICCYPLGGCLDLSRY 332

Search completed: June 4, 2003, 18:11:26
 Job time : 221.5 secs

Qy 181 GILFIYSDSTAVIICLITMFTMALMASLYVHMFMLMARLHIKRIAVLPCTGTIROGAN 240
 Db 181 GILFIYSDSTAVIICLITMFTMALMASLYVHMFMLMARLHIKRIAVLPCTGTIROGAN 240
 Qy 241 MKGAIITILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMCSIIDPL 300
 Db 241 MKGAIITILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMCSIIDPL 300
 Qy 301 IYALRSQELRKTKEIICCYPLGGCLDLSRY 332
 Db 301 IYALRSQELRKTKEIICCYPLGGCLDLSRY 332

RESULT 15
 US-09-322-695-2
 ; Sequence 2, Application US/09322695
 ; GENERAL INFORMATION:
 ; APPLICANT: Frank Lee
 ; APPLICANT: Dennis Huszar
 ; APPLICANT: Wei Gu
 ; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL
 ; FILE REFERENCE: 7853-145
 ; CURRENT APPLICATION NUMBER: US/09/322,695
 ; CURRENT FILING DATE: 1999-05-28
 ; EARLIER APPLICATION NUMBER: 08/662,560
 ; EARLIER FILING DATE: 1996-06-10
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 332
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-322-695-2

Query Match 94.6%; Score 1632.5; DB 17; Length 332;
 Best Local Similarity 95.2%; Pred. No. 1.2e-142;
 Matches 316; Conservative 6; Mismatches 9; Indels 1; Gaps 1;
 Qy 1 MNSTLQGHMTSLHFWNRSTYGOHGNATESLKGYPDGGCYEQLFVSPVEFVTLGVISLL 60
 Db 2 VNST-HRGMHTSLHLNRRSYRLHNSNASESLGKGYSDGGCYEQLFVSPVEFVTLGVISLL 60

Qy 61 ENILVIVAIKAKNLHSPMFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFVN 120
 Db 61 ENILVIVAIKAKNLHSPMFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFVN 120

Qy 121 IDNVDSVICSSLLASCSLSIAVDRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
 Db 121 IDNVDSVICSSLLASCSLSIAVDRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180

Qy 181 GILFIYSDSTAVIICLITMFTMALMASLYVHMFMLMARLHIKRIAVLPCTGTIROGAN 240
 Db 181 GILFIYSDSTAVIICLITMFTMALMASLYVHMFMLMARLHIKRIAVLPCTGTIROGAN 240

Qy 241 MKGAIITILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMCSIIDPL 300
 Db 241 MKGAIITILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMCSIIDPL 300

Qy 301 IYALRSQELRKTKEIICCYPLGGCLDLSRY 332
 Db 301 IYALRSQELRKTKEIICCYPLGGCLDLSRY 332

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 4, 2003, 18:01:21 ; Search time 36 seconds
(without alignments)
1944.050 Million cell updates/sec

Title: US-09-884-211A-4

Perfect score: 1726

Sequence: 1 MNSTLQHGHTSLHFWNRST.....FKRIICCYPLGGLDLSRY 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1006677 seqs, 210800627 residues

Total number of hits satisfying chosen parameters: 1006677

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_New:*

1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pap:*

2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pap:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pap:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pap:*

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6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pap:*

7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1639.5	95.0	332	7	US-60-443-566-3564
2	1639.5	95.0	332	7	US-60-452-680-13557
3	1639.5	95.0	332	7	US-60-455-444-4680
4	1639.5	95.0	332	7	US-60-465-241-4680
5	1638.5	94.9	332	6	US-10-225-567A-158
6	1638.5	94.9	332	6	US-10-414-521-1
7	1638.5	94.9	332	6	US-10-318-661-27
8	1632.5	94.6	332	6	US-10-413-752-2
9	1624.5	94.1	332	6	US-10-373-355-2
10	1624.5	94.1	332	6	US-60-427-882-2
11	1620.5	93.9	332	6	US-10-413-752-6
12	1592.5	92.3	332	6	US-10-288-160-16
13	1463	84.8	311	5	US-09-380-419C-3
14	1257	72.8	248	5	US-09-380-419C-4
15	1026.5	59.5	325	6	US-10-288-160-18
16	1025.5	59.4	325	1	PCT-US03-04816-40
17	1025.5	59.4	325	5	US-09-831-228-2
18	1025.5	59.4	325	6	US-10-225-567A-160
19	1025.5	59.4	325	6	US-10-369-022-40
20	982.5	56.9	360	5	US-09-949-004-341
21	982.5	56.9	360	6	US-10-219-051B-9975
22	982.5	56.9	360	7	US-60-452-680-13621
23	982.5	56.9	360	7	US-60-453-135-8500
24	982.5	56.9	360	7	US-60-453-050-8500
25	982.5	56.9	360	7	US-60-466-412-8500
26	981.5	56.9	360	5	US-09-949-004-302

Sequence 156, App
Sequence 1, Appli
Sequence 9973, Ap
Sequence 12, Appl
Sequence 60, Appl
Sequence 30, Appl
Sequence 278, App
Sequence 162, App
Sequence 60, Appl
Sequence 10677, A
Sequence 10677, A
Sequence 10677, A
Sequence 382, App
Sequence 31, Appl
Sequence 10678, A
Sequence 10678, A
Sequence 10678, A
Sequence 28, Appl
Sequence 29, Appl

27 981.5 56.9 360 6 US-10-225-567A-156
28 981.5 56.9 360 6 US-10-413-752-1
29 965 55.9 323 6 US-10-219-051B-9973
30 961 55.7 323 6 US-10-288-160-12
31 754.5 43.7 317 1 PCT-US03-02571-60
32 754.5 43.7 317 1 PCT-US03-09921-30
33 754.5 43.7 317 5 US-09-949-004-278
34 754.5 43.7 317 6 US-10-225-567A-162
35 754.5 43.7 317 6 US-10-353-690-60
36 754.5 43.7 317 7 US-60-453-135-10677
37 754.5 43.7 317 7 US-60-453-050-10677
38 754.5 43.7 317 7 US-60-466-412-10677
39 754.5 43.7 344 5 US-09-949-004-382
40 754.5 43.7 382 1 PCT-US03-09921-31
41 754.5 43.7 382 7 US-60-453-135-10678
42 754.5 43.7 382 7 US-60-453-050-10678
43 754.5 43.7 382 7 US-60-466-412-10678
44 754.5 43.7 398 1 PCT-US03-09921-28
45 754.5 43.7 398 1 PCT-US03-09921-29

ALIGNMENTS

RESULT 1

US-60-443-566-3564

; Sequence 3564, Application US/60443566

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele

; APPLICANT: BEGOVICH, Ann

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001447

; CURRENT APPLICATION NUMBER: US/60/443,566

; CURRENT FILING DATE: 2003-01-30

; NUMBER OF SEQ ID NOS: 25102

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3564

; LENGTH: 332

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-60-443-566-3564

Query Match 95.0%; Score 1639.5; DB 7; Length 332;

Best Local Similarity 95.8%; Pred. No. 1e-153;

Matches 316; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

Qy 1 MNSTLQHGHTSLHFWNRSTYQHGHNATESLGKGYPDGCGYEQLFVSPVFTLGVISLL 60
Db 2 VNST-HRGMHTSLHLNRRSSYRLHNSASESLGKGYSDGCGYEQLFVSPVFTLGVISLL 60
Qy 61 ENILVIVAIKNNKLNHSPMYFFTCISLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
Db 61 ENILVIVAIKNNKLNHSPMYFFTCISLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
Qy 121 IDNVDSVICSLLASICSLLSIADVRFYFYALQYHNIMTVRRVGIISCIWAACVTS 180
Db 121 IDNVDSVICSLLASICSLLSIADVRFYFYALQYHNIMTVRRVGIISCIWAACVTS 180
Qy 181 GILPFIYSDSTAVIICLIITFTFFTMALMASLYVHMFMLARLHKRIKRIAVLPCTGTITROGAN 240
Db 181 GILPFIYSDSTAVIICLIITFTFFTMALMASLYVHMFMLARLHKRIKRIAVLPCTGTITROGAN 240
Qy 241 MKGATITLIGVFWVCWAPFFLHIFVYISQPNPCYVCFMSHFNLYLILIMCNSIIDPL 300
Db 241 MKGATITLIGVFWVCWAPFFLHIFVYISQPNPCYVCFMSHFNLYLILIMCNSIIDPL 300
Qy 301 IYALRSQELRKTFFKEIICCYPLGGLDLSRY 332
Db 301 IYALRSQELRKTFFKEIICCYPLGGLDLSRY 332

RESULT 2

US-60-452-680-13557

; Sequence 13557, Application US/60452680

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele

; APPLICANT: GRUPE, Andrew

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; FILE REFERENCE: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/60/452,680

; CURRENT FILING DATE: 2003-03-07

; NUMBER OF SEQ ID NOS: 116213

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13557

; LENGTH: 332

; TYPE: PRT

; ORGANISM: Homo sapiens

US-60-452-680-13557

Query Match

Best Local Similarity 95.0%; Score 1639.5; DB 7; Length 332;

Matches 318; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

QY 1 MNSTLQHGHTSLHFWNRSTYQHGHNATESLGKGYDGGCYQLFVSPVEFVTLGVISLL 60

Db 2 VNST-HRGHTSLHLNRSYRLHSNASESLGKGYSDGGCYQLFVSPVEFVTLGVISLL 60

QY 61 ENILVIAIAKKNLHSPMYFFICSIAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120

Db 61 ENILVIAIAKKNLHSPMYFFICSIAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120

QY 121 INVIDSVTCSSLLASICSLLSIADRYFTFYALQYHNMVRRVGGIISCIWAACVTS 180

Db 121 INVIDSVTCSSLLASICSLLSIADRYFTFYALQYHNMVRRVGGIISCIWAACVTS 180

QY 181 GILFIYSDSTAVIICLTMTFMTLMALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 240

Db 181 GILFIYSDSTAVIICLTMTFMTLMALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 240

QY 241 MKGATITLILIGVVCWAPFFLHLFIYISCPQNPYCVCFMSHFENLYLILIMCNSIIDPL 300

Db 241 MKGATITLILIGVVCWAPFFLHLFIYISCPQNPYCVCFMSHFENLYLILIMCNSIIDPL 300

QY 301 IYALRSQELRKTKEIICCYPLGGCLDLSRY 332

Db 301 IYALRSQELRKTKEIICCYPLGGCLDLSRY 332

RESULT 3

US-60-455-444-4680

; Sequence 4680, Application US/60455444

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele

; APPLICANT: BEGOVICH, Ann

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; FILE REFERENCE: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/60/455,444

; CURRENT FILING DATE: 2003-03-18

; NUMBER OF SEQ ID NOS: 50986

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4680

; LENGTH: 332

; TYPE: PRT

; ORGANISM: Homo sapiens

US-60-455-444-4680

Query Match

Best Local Similarity 95.0%; Score 1639.5; DB 7; Length 332;

Matches 318; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

QY 1 MNSTLQHGHTSLHFWNRSTYQHGHNATESLGKGYDGGCYQLFVSPVEFVTLGVISLL 60

Db 2 VNST-HRGHTSLHLNRSYRLHSNASESLGKGYSDGGCYQLFVSPVEFVTLGVISLL 60

```
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO:158
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-158

Query Match          94.9%; Score 1638.5; DB 6; Length 332;
Best Local Similarity 95.5%; Pred. No. 1.3e-153;
Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 1 MNSTLQGMHTSLHFNWRSYTGQGNATESLGKGYPDGGCYEQLFVSPVEFVTLGVISLL 60
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2 VNST-HRGMHTSLHLNRRSSYRLHSNASESLGKGYSDGGCYEQLFVSPVEFVTLGVISLL 60
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNGSETIVITLLNSTDTDAQSFTVN 120
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNGSETIVITLLNSTDTDAQSFTVN 120
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 IDNVDSVICSSLLASICSLLSIAVDRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 IDNVDSVICSSLLASICSLLSIAVDRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 GILFIYSDSTAVIICLITMFTTMLMASLYVHMFMLMARLHIKRIAVLPCTGTIROGAN 240
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 GILFIYSDSTAVIICLITMFTTMLMASLYVHMFMLMARLHIKRIAVLPCTGTIROGAN 240
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 MKGAIITLILIGVFWCWAPEFLHLIFYISCPNPYCVCFMSHFNLYLILIMCNSIIDPL 300
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 MKGAIITLILIGVFWCWAPEFLHLIFYISCPNPYCVCFMSHFNLYLILIMCNSIIDPL 300
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 IYALRSQELRKTEKEIICCCYPLGGLCDLSSRY 332
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 IYALRSQELRKTEKEIICCCYPLGGLCDLSSRY 332
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 6
US-10-414-521-1
; Sequence 1, Application US/10414521
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Colson, Anny-Odile
; APPLICANT: Mieling, Glen
; TITLE OF INVENTION: Three Dimensional Coordinates of Melanocortin-4 Receptors
; FILE REFERENCE: 9207
; CURRENT APPLICATION NUMBER: US/10/414,521
; CURRENT FILING DATE: 2003-04-15
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-414-521-1

Query Match          94.9%; Score 1638.5; DB 6; Length 332;
Best Local Similarity 95.5%; Pred. No. 1.3e-153;
Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 1 MNSTLQGMHTSLHFNWRSYTGQGNATESLGKGYPDGGCYEQLFVSPVEFVTLGVISLL 60
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
Db 2 VNST-HRGMHTSLHLNRRSSYRLHSNASESLGKGYSDGGCYEQLFVSPVEFVTLGVISLL 60
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNGSETIVITLLNSTDTDAQSFTVN 120
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNGSETIVITLLNSTDTDAQSFTVN 120
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 IDNVDSVICSSLLASICSLLSIAVDRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 IDNVDSVICSSLLASICSLLSIAVDRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 GILFIYSDSTAVIICLITMFTTMLMASLYVHMFMLMARLHIKRIAVLPCTGTIROGAN 240
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 GILFIYSDSTAVIICLITMFTTMLMASLYVHMFMLMARLHIKRIAVLPCTGTIROGAN 240
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 MKGAIITLILIGVFWCWAPEFLHLIFYISCPNPYCVCFMSHFNLYLILIMCNSIIDPL 300
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 MKGAIITLILIGVFWCWAPEFLHLIFYISCPNPYCVCFMSHFNLYLILIMCNSIIDPL 300
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 IYALRSQELRKTEKEIICCCYPLGGLCDLSSRY 332
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 IYALRSQELRKTEKEIICCCYPLGGLCDLSSRY 332
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
US-10-318-661-27
; Sequence 27, Application US/10318661
; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; TITLE OF INVENTION: Superiorly By Synthetic Ligand
; FILE REFERENCE: UCAL-049CIP2
; CURRENT APPLICATION NUMBER: US/10/318,661
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 09/341,446
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-318-661-27

Query Match          94.9%; Score 1638.5; DB 6; Length 332;
Best Local Similarity 95.5%; Pred. No. 1.3e-153;
Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 1 MNSTLQGMHTSLHFNWRSYTGQGNATESLGKGYPDGGCYEQLFVSPVEFVTLGVISLL 60
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2 VNST-HRGMHTSLHLNRRSSYRLHSNASESLGKGYSDGGCYEQLFVSPVEFVTLGVISLL 60
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNGSETIVITLLNSTDTDAQSFTVN 120
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNGSETIVITLLNSTDTDAQSFTVN 120
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 IDNVDSVICSSLLASICSLLSIAVDRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 IDNVDSVICSSLLASICSLLSIAVDRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 GILFIYSDSTAVIICLITMFTTMLMASLYVHMFMLMARLHIKRIAVLPCTGTIROGAN 240
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 GILFIYSDSTAVIICLITMFTTMLMASLYVHMFMLMARLHIKRIAVLPCTGTIROGAN 240
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 MKGAIITLILIGVFWCWAPEFLHLIFYISCPNPYCVCFMSHFNLYLILIMCNSIIDPL 300
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 MKGAIITLILIGVFWCWAPEFLHLIFYISCPNPYCVCFMSHFNLYLILIMCNSIIDPL 300
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 IYALRSQELRKTEKEIICCCYPLGGLCDLSSRY 332
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 IYALRSQELRKTEKEIICCCYPLGGLCDLSSRY 332
   :||| ||||| ||||| : ||| ||||| ||||| ||||| ||||| ||||| |||||
```


Qy 181 GILFIYSDSTAVIICLITMFTMLMALMASLYVHMFLMARLHKRIARVLPCTGTGIRQGAN 240
Db 181 GILFIYSDSSAVIICLITMFTMLMALMASLYVHMFLMARLHKRIARVLPCTGTGIRQGAN 240
Qy 241 MKGAIITLILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
Db 241 MKGAIITLILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
Qy 301 IYALRSQELRKTKEIICCYPLGGLCDLSRY 332
Db 301 IYALRSQELRKTKEIICCYPLGGLCDLSRY 332

RESULT 11
US-10-413-752-6
; Sequence 6, Application US/10413752
; GENERAL INFORMATION:
; APPLICANT: Frank Lee
; APPLICANT: Dennis Huszar
; APPLICANT: Wei Gu
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL
; FILE REFERENCE: 7953-145
; CURRENT APPLICATION NUMBER: US/10/413,752
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/09/322,695
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/662,560
; PRIOR FILING DATE: 1996-06-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-413-752-6

Query Match 93.9%; Score 1620.5; DB 6; Length 332;
Best Local Similarity 94.3%; Pred. No. 7.8e-152;
Matches 313; Conservative 7; Mismatches 11; Indels 1; Gaps 1;
Qy 1 MNSTLQHGHTSLHFNWNRSTYGOHGNATESLKGKYPDGCGYEQLFVSPVEVFTLGVISLL 60
Db 2 VNST-HRGMHTSLHLNRRSSVRLHNSASESLGKGYSDGCGYEQLFVSPVEVFTLGVISLL 60
Qy 61 ENILVIVAIAKNNLHSPMYFFTCISLAVADMVSVNSGSETIVITLLNSTDTDAQSTVN 120
Db 61 ENILVIVAIAKNNLHSPMYFFTCISLAVADMVSVNSGSETIVITLLNSTDTDAQSTVN 120
Qy 121 IDNVDSVICSSLLASCSLLSIADVDYFTIFYALQYHNMTVRRVGIIISCIWAACVTS 180
Db 121 IDNVDSVICSSLLASCSLLSIADVDYFTIFYALQYHNMTVRRVGIIISCIWAACVTS 180
Qy 181 GILFIYSDSTAVIICLITMFTMLMALMASLYVHMFLMARLHKRIARVLPCTGTGIRQGAN 240
Db 181 GILFIYSDSSAVIICLITMFTMLMALMASLYVHMFLMARLHKRIARVLPCTGTGIRQGAN 240
Qy 241 MKGAIITLILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
Db 241 MKGAIITLILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
Qy 301 IYALRSQELRKTKEIICCYPLGGLCDLSRY 332
Db 301 IYALRSQELRKTKEIICCYPLGGLCDLSRY 332

RESULT 12
US-10-288-160-16
; Sequence 16, Application US/10288160
; GENERAL INFORMATION:
; APPLICANT: Cone, Roger D
; Fan, Wei
; Boston, Bruce A

; Kesterton, Robert A
; Lu, Dongsi
; Chen, Wenbiao
; TITLE OF INVENTION: Methods and Reagents for Discovering and
; Using Mammalian Melanocortin Receptor Agonists and Antag
; To Modulate Feeding Behavior in Animals
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/288,160
; FILING DATE: 05-Nov-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: US/08/706,281
; FILING DATE: 04-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Noonan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 96,886
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-288-160-16

Query Match 92.3%; Score 1592.5; DB 6; Length 332;
Best Local Similarity 93.4%; Pred. No. 4.6e-149;
Matches 310; Conservative 7; Mismatches 14; Indels 1; Gaps 1;
Qy 1 MNSTLQHGHTSLHFNWNRSTYGOHGNATESLKGKYPDGCGYEQLFVSPVEVFTLGVISLL 60
Db 2 VNST-HRGMHTSLHLNRRSSVRLHNSASESLGKGYSDGCGYEQLFVSPVEVFTLGVISLL 60
Qy 61 ENILVIVAIAKNNLHSPMYFFTCISLAVADMVSVNSGSETIVITLLNSTDTDAQSTVN 120
Db 61 ENILVIVAIAKNNLHSPMYFFTCISLAVADMVSVNSGSETIVITLLNSTDTDAQSTVN 120
Qy 121 IDNVDSVICSSLLASCSLLSIADVDYFTIFYALQYHNMTVRRVGIIISCIWAACVTS 180
Db 121 IDNVDSVICSSLLASCSLLSIADVDYFTIFYALQYHNMTVRRVGIIISCIWAACVTS 180
Qy 181 GILFIYSDSTAVIICLITMFTMLMALMASLYVHMFLMARLHKRIARVLPCTGTGIRQGAN 240
Db 181 GILFIYSDSSAVIICLITMFTMLMALMASLYVHMFLMARLHKRIARVLPCTGTGIRQGAN 240
Qy 241 MKGAIITLILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
Db 241 MKGAIITLILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
Qy 301 IYALRSQELRKTKEIICCYPLGGLCDLSRY 332
Db 301 IYALRSQELRKTKEIICCYPLGGLCDLSRY 332

RESULT 13

US-09-380-419C-3
; Sequence 3, Application US/09380419C
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max F.
; APPLICANT: Larsen, Neils
; APPLICANT: Kim, Kwan
; TITLE OF INVENTION: Melanocortin-4 Receptor Gene and Use as a Genetic Marker for Fat
; TITLE OF INVENTION: Weight Gain, and/or Feed Consumption in Animals
; FILE REFERENCE: ISURF 2413
; CURRENT APPLICATION NUMBER: US/09/380,419C
; CURRENT FILING DATE: 2000-07-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (298)..(298)
; OTHER INFORMATION: "X" can be any amino acid
US-09-380-419C-3

Query Match 84.8%; Score 1463; DB 5; Length 311;
Best Local Similarity 98.3%; Pred. No. 2.6e-136;
Matches 285; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 43 QLFVSPVFTVLGVISLLENILVIAIAKKNLHSPMYFFICSLAVADMVSVSNGSETI 102
Db 1 QLFVSPVFTVLGVISLLENILVIAIAKKNLHSPMYFFICSLAVADMVSVSNGSETI 60

QY 103 VITLLNSTDTDAQSFVNIDNVDVSVCSLLASICSLSIAVDVFTTFYALQYHNIMT 162
Db 61 IITLLNSTDTDAQSFVNIDNVDVSVCSLLASICSLSIAVDVFTTFYALQYHNIMT 120

QY 163 VRVGTIISCIWAACVSGILFTIYSDSTAVIICLTMTFTMLMASLYVHMFMLARLH 222
Db 121 VRVGTIISCIWAACVSGILFTIYSDSTAVIICLTMTFTMLMASLYVHMFMLARLH 180

QY 223 IKRIAVLPGTGIRQGANMKGAITTLIGVFVVCWAPFHLHIFYISCPQNPYCVCFMS 282
Db 181 IKRIAVLPGTGIRQGANMKGAITTLIGVFVVCWAPFHLHIFYISCPQNPYCVCFMS 240

QY 283 HFNLYILMCSNIIDPLIYALRSQELRTFKFICCYPLGGCLDLSRY 332
Db 241 HFNLYILMCSNIIDPLIYALRSQELRTFKFICCYPLGGCLDLSRY 290

RESULT 14
US-09-380-419C-4
; Sequence 4, Application US/09380419C
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max F.
; APPLICANT: Larsen, Neils
; APPLICANT: Kim, Kwan
; TITLE OF INVENTION: Melanocortin-4 Receptor Gene and Use as a Genetic Marker for Fat
; TITLE OF INVENTION: Weight Gain, and/or Feed Consumption in Animals
; FILE REFERENCE: ISURF 2413
; CURRENT APPLICATION NUMBER: US/09/380,419C
; CURRENT FILING DATE: 2000-07-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-380-419C-4

Query Match 72.8%; Score 1257; DB 5; Length 248;
Best Local Similarity 97.6%; Pred. No. 4.5e-116;
Matches 242; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 73 KNLHSPMYFFICSLAVADMVSVSNGSETIVITLLNSTDTDAQSFVNIDNVDVSVCS 132

Db 1 KNLHSPMYFFICSLAVADMVSVSNGSETIVITLLNSTDTDAQSFVNIDNVDVSVCS 60

QY 133 LLASICSLSIAVDVFTTFYALQYHNIMTVRRVGIISCIWAACVSGILFTIYSDSTA 192
Db 61 LLASICSLSIAVDVFTTFYALQYHNIMTVRRVGIISCIWAACVSGILFTIYSDSTA 120

QY 193 VIICLTMTFTMLMASLYVHMFMLARLHMKRIAVLPGTGIRQGANMKGAITTLIG 252
Db 121 VIICLTMTFTMLMASLYVHMFMLARLHMKRIAVLPGTGIRQGANMKGAITTLIG 180

QY 253 VFVVCWAPFHLHIFYISCPQNPYCVCFMSHFNLYILMCSNIIDPLIYALRSQELRKT 312
Db 181 VFVVCWAPFHLHIFYISCPQNPYCVCFMSHFNLYILMCSNIIDPLIYALRSQELRKT 240

QY 313 FKEIICCY 320
Db 241 FKEIICCY 248

RESULT 15
US-10-288-160-18
; Sequence 18, Application US/10288160
; GENERAL INFORMATION:
; APPLICANT: Cone, Roger D
; APPLICANT: Fan, Wei
; APPLICANT: Boston, Bruce A
; APPLICANT: Kesterton, Robert A
; APPLICANT: Lu, Dongsi
; APPLICANT: Chen, Wenbiao
TITLE OF INVENTION: Methods and Reagents for Discovering and
Using Mammalian Melanocortin Receptor Agonists and Antag
To Modulate Feeding Behavior in Animals

NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSER: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/288,160
FILING DATE: 05-Nov-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/706,281
FILING DATE: 04-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Noonan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 96,886
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-288-160-18

Query Match 59.5%; Score 1026.5; DB 6; Length 325;
Best Local Similarity 66.8%; Pred. No. 3.9e-93;
Matches 195; Conservative 43; Mismatches 53; Indels 1; Gaps 1;

Qy	42	EQLFVSEVFTLGVISLLENILVIVAIAKNKLNHSPWPFICSLAVADMLVSVNGSET	101
Db	34	EEMGIAVEVELTGLVSLLENILVIGAIVKKNLHSPWPFVGS LAVADMLVSMNAWET	93
Qy	102	IVITLLNSTD-TDAQSFVNIDNVDSVICSSLLASTCSLSTIAVDRYFTIFYALQYHNI	160
Db	94	VTIYLLNKKHLVIADTEVRHIDNVFDSMICISVVASMCSSLIAIAVDRYITIFYALRYHHI	153
Qy	161	MTVRRVGIILSCIWAACTVSGILFIYISDSTAVIICLITWFFTMALMASLYVHMFILMAR	220
Db	154	MTARRSGVITACIWTFCISGIVFIYIESKYVICLISMFMTLFFWVSLYIHMFLIAR	213
Qy	221	LHIKRIAVLPGTGTIRQCANMKGAITLTILIGVFCWAPFFLHLIFYISCPQNPYCVCF	280
Db	214	NHVKRIAASPRYNSVRQRTSMKGAITLTMLLGIFIVCWSPEFFLHLIIMISCPQNPYCSF	273
Qy	281	MSHFNLYLILIMCNSIIDPLIYALRSQELRKTEIICCYPLGGLCDLSSRY	332
Db	274	MSYFNMYLILIMCNSVIDPLIYALRSQEMRRTKEIIVCCHGFRPRCRLGGY	325

Search completed: June 4, 2003, 18:12:46
Job time : 37 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 4, 2003, 18:12:51 ; Search time 26 seconds
(without alignments)
1227.563 Million cell updates/sec

Title: us-09-884-211a-4

Perfect score: 1726

Sequence: 1 MNSTLQHGHTSLHFWNRST.....FKRIICYPGLGGLDLSRY 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1632.5	94.6	332	2 A57055	melanocortin recep
2	1070	62.0	215	2 B57055	melanocortin-4 rec
3	1041	60.3	325	2 JC2193	melanocortin recep
4	1023.5	59.3	372	2 I49008	melanocortin-5 rec
5	1022.5	59.2	325	2 JC5592	melanocortin 5 rec
6	1003.5	58.1	325	2 JN0764	melanocortin recep
7	994	57.6	323	2 S43850	melanocortin 3 rec
8	987.5	57.2	360	2 B46647	melanocortin recep
9	965	55.9	323	2 S36636	melanocortin recep
10	962.5	55.8	325	2 I46416	melanocyte-stimula
11	830.5	48.1	314	2 S71420	melanocortin 1 rec
12	817.5	47.4	314	2 S70005	melanocortin 1 rec
13	770	44.6	317	2 S45708	MSH receptor - bov
14	766	44.4	317	2 T12055	melanocyte stimula
15	752.5	43.6	315	2 S25581	melanocyte-stimula
16	751.5	43.5	317	2 S29204	melanotropin recep
17	724	41.9	297	2 S42767	adrenocorticotropi
18	723	41.9	297	2 C43265	adrenocorticotropi
19	721	41.8	296	2 I52326	adrenocorticotropi
20	718	41.6	296	2 JC4046	adrenocorticotropi
21	700	40.6	297	2 I45849	gene ACTH receptor
22	358.5	20.8	364	2 JC5293	lysophosphatidic a
23	329.5	19.1	383	2 I53870	Egfr-1 orphan recep
24	327	18.9	362	2 JC7559	sphingosine 1-phos
25	323	18.7	317	2 JC2335	melanocortin recep
26	320.5	18.6	381	2 A35300	G protein-coupled
27	316.5	18.3	330	2 A55689	G protein-coupled
28	305	17.7	352	2 JC1465	probable G protein
29	302.5	17.5	330	2 S40454	G protein-coupled

RESULT 1

A57055 melanocortin receptor 4 - human

C:Species: Homo sapiens (man)

C>Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 24-Sep-1999

C:Accession: A57055; A47111

R:Mountjoy, K.G.; Mortrud, M.T.; Low, M.J.; Simerly, R.B.; Cone, R.D.

Mol. Endocrinol. 8, 1298-1308, 1994

A:Title: Localization of the melanocortin-4 receptor (MC4-R) in neuroendocrine and au

A:Reference number: A57055; MUID:95157557; PMID:7854347

A:Accession: A57055

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-332 <MOU>

A:Cross-references: GB:S77415; NID:g998456; PIDN:AA33341.1; PID:g998457

R:Gantz, I.; Miwa, H.; Konda, Y.; Shimoto, Y.; Tashiro, T.; Watson, S.J.; DelValle, J

J. Biol. Chem. 268, 15174-15179, 1993

A:Title: Molecular cloning, expression, and gene localization of a fourth melanocorti

A:Reference number: A47111; MUID:93315499; PMID:8392067

A:Accession: A47111

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-168, 'I', 170-332 <GAN>

A:Cross-references: GB:L08603; NID:g291977; PIDN:AAA35791.1; PID:g291978

C:Genetics:

A:Gene: GDB:MC4R

A:Cross-references: GDB:203939; OMIM:155541

A:Map position: 20q13.2-20q13.3

C:Superfamily: melanocortin receptor

C:Keywords: hormone receptor

Query Match 94.6%; Score 1632.5; DB 2; Length 332;

Best Local Similarity 95.2%; Pred. No. 3.3e-126;

Matches 316; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Qy 1 MNSTLQHGHTSLHFWNRSTYQHGHNATESLGKGYPDGCGYEQLFVSPVEVFTLGVISLL 60

Db 2 VNST-HRGHTHTSLHFWNRSTYRLHNSASESLGKGYSDGCGYEQLFVSPVEVFTLGVISLL 60

Qy 61 ENILVIVAIARKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFIVN 120

Db 61 ENILVIVAIARKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFIVN 120

Qy 121 IDNVDSVICSLLASCSLLSIADVRYFTTFYALQYHNIMTVRRVGIISCIWAACVTS 180

Db 121 IDNVDSVICSLLASCSLLSIADVRYFTTFYALQYHNIMTVRRVGIISCIWAACVTS 180

Qy 181 GILPIIYSDTAVIICLITMFFTMALMASLYVMFLMARLHRIKRIAVLPCTGTIRQGAN 240

Db 181 GILPIIYSDTAVIICLITMFFTMALMASLYVMFLMARLHRIKRIAVLPCTGTIRQGAN 240

Qy 241 MKGAIITLILIGVFVVCWAPFFLLIFVISCQPONPYCVCFMSHENLVILIMCNSIIDPL 300

ALIGNMENTS

Db 241 MKGATITLIGVFWVWAPFFHLFIYISCPNYPVCVCFMSHFNLYLILMCSNIDPL 300
QY 301 IYALRSQELRKTEIKCIICCPYPLGGLDLSRY 332
Db 301 IYALRSQELRKTEIKCIICCPYPLGGLDLSRY 332
RESULT 2
B57055
melanocortin-4 receptor - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 07-May-1999
C:Accession: B57055
R:Mountjoy, K.G.; Mørtud, M.T.; Low, M.J.; Simerly, R.B.; Cone, R.D.
Mol. Endocrinol. 8, 1298-1308, 1994
A:Title: Localization of the melanocortin-4 receptor (MC4-R) in neuroendocrine and autonomic nervous system of the rat.
A:Reference number: A57055; MUID:95157557; PMID:7854347
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-215 <MOU>
C:Superfamily: melanocortin receptor

Query Match 62.0%; Score 1070; DB 2; Length 215;
Best Local Similarity 96.3%; Pred. No. 2.3e-80;
Matches 207; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 78 PMYFFICSLAVADMLVSVNGSETIVITLLNSTDDAQSTFTVNDVDSVCSLLASI 137
Db 1 PMYFFICSLAVADMLVSVNGSETIVITLLNSTDDAQSTFTVNDVDSVCSLLASI 60
QY 138 CSLLSTAVDRYFTIFALYGHNIMTVRRVGIISCIWAACVSGILFIYSDSTAVIICL 197
Db 61 CSLLSTAVDRYFTIFALYGHNIMTVRRVGIISCIWAACVSGILFIYSDSTAVIICL 120
QY 198 ITMFFMLALMASLYVHMFMLARKHRIKRIAVLPCTGTIRQANMKGAITLTILIGVFVVC 257
Db 121 ITMFFMLALMASLYVHMFMLARKHRIKRIAVLPCTGTIRQANMKGAITLTILIGVFVVC 180
QY 258 WAPFFLHLFIYISCPNYPVCVCFMSHFNLYLILIM 292
Db 181 WAPFFLHLFIYISCPNYPVCVCFMSHFNLYLILIM 215

RESULT 3
JC2193
melanocortin receptor, MC5 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 24-Sep-1999
C:Accession: JC2193
R:Griffon, N.; Mignon, V.; Facchinetti, P.; Diaz, J.; Schwartz, J.C.; Sokoloff, P.
Biochem. Biophys. Res. Commun. 200, 1007-1014, 1994
A:Title: Molecular cloning and characterization of the rat fifth melanocortin receptor.
A:Reference number: JC2193; MUID:94234987; PMID:8179577
A:Accession: JC2193
A:Molecule type: DNA
A:Residues: 1-325 <GR1>
A:Cross-references: GB:L27081; NID:9435606; PIDN:AAAA1577.1; PID:9435607
C:Superfamily: melanocortin receptor
C:Keywords: G protein-coupled receptor; receptor; transmembrane protein
F:37-63/Domain: transmembrane #status predicted <TM1>
F:73-98/Domain: transmembrane #status predicted <TM2>
F:117-138/Domain: transmembrane #status predicted <TM3>
F:159-179/Domain: transmembrane #status predicted <TM4>
F:193-211/Domain: transmembrane #status predicted <TM5>
F:240-263/Domain: transmembrane #status predicted <TM6>
F:276-297/Domain: transmembrane #status predicted <TM7>

Query Match 60.3%; Score 1041; DB 2; Length 325;
Best Local Similarity 65.0%; Pred. No. 8.1e-78;
Matches 202; Conservative 45; Mismatches 60; Indels 4; Gaps 3;

QY 26 NATES--LGKGYPD-GGCYBQLEFVSPEVFTLGLVILLENILVIVAIKKNLHSPMYFF 82
Db 15 NASEDNLTGQNVNKKSSACEDMGIAVEVFTLGLVILLENILVIVAIKKNLHSPMYFF 74
QY 83 ICSLAVADMLVSVNGSETIVITLLNSTD-TDAQSTFTVNDVDSVCSLLASCSLL 141
Db 75 VGS LAVADMLVSVNSNAWETITTYLINNHKVVIADTFVRHIDNVFDSMICSIVVASMCSLL 134
QY 142 STAVDRYFTIFALYGHNIMTVRRVGIISCIWAACVSGILFIYSDSTAVIICLTMF 201
Db 135 AIADRYITIFALYGHNIMTVRRVGIISCIWAACVSGILFIYSDSTAVIICLTMF 194
QY 202 FTMLALMASLYVHMFMLARKHRIKRIAVLPCTGTIRQANMKGAITLTILIGVFVVCWAPF 261
Db 195 FTMLFVSVLYIHMFLLARNHVKRIASPRYSNVRQASMKGAITLTMLGIIIVCWSPF 254
QY 262 FTHLPIYISCPNYPVCVCFMSHFNLYLILMCSNIDPLIYALRSQELRKTEIKCIICYP 321
Db 255 FTHLPIYISCPNYPVCVCFMSHFNLYLILMCSNIDPLIYALRSQELRKTEIKCIICCHG 314
QY 322 LGGLCDLSRY 332
Db 315 FRRTCTLLGRY 325
RESULT 4
I49008
melanocortin-5 receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C:Accession: I49008; A54245; JC2244
R:Fathi, Z.; Iben, L.G.; Parker, E.M.
Neurochem. Res. 20, 107-113, 1995
A:Title: Cloning, expression, and tissue distribution of a fifth melanocortin receptor.
A:Reference number: I49008; MUID:95258173; PMID:7739752
A:Accession: I49008
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-372 <RES>
A:Cross-references: EMBL:U08354; NID:9522165; PIDN:AAA76585.1; PID:9522166
R:Labbe, O.; Desarnaud, F.; Eggerickx, D.; Vassart, G.; Parmentier, M.
Biochemistry 33, 4543-4549, 1994
A:Title: Molecular cloning of a mouse melanocortin 5 receptor gene widely expressed in the brain.
A:Reference number: A54245; MUID:94213827; PMID:8161509
A:Accession: A54245
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 48-120, F', 122-372 <LAB>
A:Cross-references: GB:X76295; NID:9498973; PIDN:CAA53943.1; PID:9498974
A:Experimental source: clone HGMP01B
A:Note: sequence extracted from NCBI backbone (NCBIP:145988)
R:Gantz, I.; Shimoto, Y.; Konda, Y.; Miwa, H.; Dickinson, C.J.; Yamada, T.
Biochem. Biophys. Res. Commun. 200, 1214-1220, 1994
A:Title: Molecular cloning, expression, and characterization of a fifth melanocortin receptor.
A:Reference number: JC2244; MUID:94241974; PMID:8185570
A:Accession: JC2244
A:Molecule type: DNA
A:Residues: 48-372 <GAN>
A:Cross-references: GB:L22527; NID:9468377; PIDN:AAA21337.1; PID:9468378
C:Comment: This protein responds to melanocortins with an increase in intracellular cAMP.
C:Superfamily: melanocortin receptor
C:Keywords: receptor; transmembrane protein
F:84-109/Domain: transmembrane #status predicted <TM1>
F:121-144/Domain: transmembrane #status predicted <TM2>
F:164-185/Domain: transmembrane #status predicted <TM3>
F:206-226/Domain: transmembrane #status predicted <TM4>
F:232-257/Domain: transmembrane #status predicted <TM5>
F:287-310/Domain: transmembrane #status predicted <TM6>
F:324-344/Domain: transmembrane #status predicted <TM7>

Query Match 59.3%; Score 1023.5; DB 2; Length 372;
Best Local Similarity 66.4%; Pred. No. 2.5e-76;
Matches 194; Conservative 44; Mismatches 53; Indels 1; Gaps 1;

Qy	42	EQLFVSPV	EVFTLVGLV	ISLLENILV	IVATAK	NNLHSP	MYFFICS	LAVADML	VSNGS	SET	10														
Db	81	EEMGIA	VEVFTLVGL	VSLLENIL	VIGATK	NNLHSP	MYFVGV	LAVADML	VSMSNA	WET	14														
Qy	102	IVITLL	NSTD	-TDAQS	FTVND	NVD	SVICSS	LLASTC	SLSI	AVDRY	FTTFYALQY	HNI	160												
Db	141	VTIYLL	NANKHL	VIADT	VRHID	NVDF	SMICIS	VS	VASMC	SLAI	AVDRY	ITTFYALRY	HHI	200											
Qy	161	MTVRRV	GLIIIS	WAAC	TVSGIL	FIITY	SDSTA	VAVI	CIIT	MTFET	MLAL	MSLYV	HMF	220											
Db	201	MTARRS	GVIIAC	ITWFC	ISCGI	VIFII	YKSV	YVCI	ILSM	FETM	LFV	SVLSY	IHM	260											
Qy	221	LHKRI	AVLP	OTGT	IROG	ANKK	GAIT	LITIL	GVFV	VCW	APFL	HLIF	YIS	CPNQ	VCVF	280									
Db	261	NHVKRI	AA	SPRYS	VRQRT	SKGA	ITL	MLGIG	IFV	CS	PFL	HLIL	MIS	CPNQ	VCSCF	320									
Qy	281	MSHEN	LYLIL	TMCS	IIDPL	IYAL	RSQ	ELRT	FKFE	ICCY	PLGG	ICD	LS	RSY	332										
Db	321	MSYFN	MYLIL	TMCS	VIDPL	IYAL	RSQ	MRRT	FKFE	IVC	HGR	FR	CR	LLGGY	372										
RESULT 5																									
JC5592																									
melanocortin 5 receptor - human																									
C:Species: Homo sapiens (man)																									
C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 07-May-1999																									
C:Accession: JC5592																									
R:Fraendberg, P.A.; Xu, X.; Chhajlani, V.																									
Biochem. Biophys. Res. Commun. 236, 489-492, 1997																									
A:Title: Glutamine-235 and arginine-272 in human melanocortin 5 receptor deter																									
A:Reference number: JC5592; MUID:97382462; PMID:9240466																									
A:Accession: JC5592																									
A:Molecule type: protein																									
A:Residues: 1-325 <PR2>																									
C:Comment: This protein is the melanocortin receptor with low affinity towards																									
C:Superfamily: melanocortin receptor																									
F:37-61/Domain: transmembrane #status predicted <TM1>																									
F:77-100/Domain: transmembrane #status predicted <TM2>																									
F:115-138/Domain: transmembrane #status predicted <TM3>																									
F:156-179/Domain: transmembrane #status predicted <TM4>																									
F:187-210/Domain: transmembrane #status predicted <TM5>																									
F:240-263/Domain: transmembrane #status predicted <TM6>																									
F:274-297/Domain: transmembrane #status predicted <TM7>																									
Query Match 59.2%; Score 1022.5; DB 2; Length 325;																									
Best Local Similarity 62.0%; Pred. No. 2.7e-76;																									
Matches 207; Conservative 42; Mismatches 77; Indels 13; Gaps 5																									
Qy	1	MNST	LQGM	HTSL	HFWR	NRSTY	GQHG	NAT	-	ESL	KGYP	DGG	CYEOL	FVS	PEV	FTLV	GLVIS	58							
Db	1	MNSSFH	-----	LHFL	DNL	NAT	EGN	ISG	PV	NK	NSSP	-	-	C	EDM	GL	AVE	VFL	GLVIS	50					
Qy	59	LLENIL	VIVA	TA	KNNL	HSP	MYFF	ICS	LAV	ADML	VS	NGS	SET	YIT	LL	NST	D	-TDAQ	SF	117					
Db	51	LLENIL	VIG	A	VK	NNL	HSP	MYF	FV	GV	SL	AV	ADML	VS	MS	SSA	WET	IT	YLL	NNK	HL	VI	AD	F	110
Qy	118	TVND	NVD	SVIC	SS	LLAST	C	SLSI	AVDR	Y	FTTF	YAL	QY	NI	NI	MT	VRR	V	GVII	IS	CI	WA	C	177	
Db	111	VRHID	NVDF	SMIC	IS	VV	ASMC	SLAI	AVDR	Y	ITTF	YAL	AY	HHI	MT	FARR	S	GAI	IAG	I	WA	C	170		
Qy	178	TVSGIL	FI	ITY	SD	STA	VAVI	CI	IT	MT	FET	ML	AL	MS	LYV	HMF	LA	RH	KRI	AV	LP	GT	IR	Q	237
Db	171	TGCGI	VFI	LS	Y	SE	STV	IV	CL	IS	ME	FAM	LF	VS	YI	HMF	LA	R	TH	VK	RI	AL	P	G	230
Qy	238	GANNK	GAIT	L	TIL	GV	FV	VCW	AP	FL	HL	IF	YIS	CP	NQ	PY	CV	CF	SH	FN	LY	L	I	L	297
Db	231	RTSMQ	AV	T	MLG	IG	IF	V	CS	P	FL	HL	T	ML	S	C	PQ	N	L	S	C	R	F	N	290
Qy	298	DPLI	YAL	RSQ	EL	RT	FK	FE	IC	CY	P	L	G	G	I	C	D	L	S	R	331				
Db	291	DPLI	YAL	RSQ	MR	KT	FK	FE	IC	CR	G	R	F	I	A	C	S	P	R	324					

[illegible]

Db	1	MNSFPH-----LHFLDLGLNATGNNLS-GLSVRNASSPC-EDMGIAVEVFLALGJLSL	52
QY	61	ENILVIAIAKNNKHSPMYFFICSLAVADMLYSVNSGSETIVITLL-NSTDTDQAQSFV	119
Db	53	ENILVIGAIRNRNLHPIPVFVGLSADVADMLYSLSNFWEITITVLLTNKHLVMADASVR	112
QY	120	NIDNVIDSVCSSLASLASCLSLTAADRYETTFVALQYHNIMVRVGGIISCIWAACV	179
Db	113	HLDNVFDWICISVVASMCSLATAADRYVTIFCLRKYQIRIMTGRSGAIIAGIWAFCWS	172
QY	180	SGILFIYSDSTAVIICLIUTMFTMLALMASLYVHMFMLARLHKIRAVLPGTGTIRQGA	239
Db	173	CGTVFIVYESTYVVVCLIAMFLTMLLIMASLATHMPELLARTHVRRIAALPGHSSVRQT	232
QY	240	NMKGAITITILIGVFWCWAPEFHLHFIYISCPONPYCVCFMGSFNLYLLILMCSNIDP	299
Db	233	GVKGAITLMLGLVFIICWAFPEFHLHILMISCFQNLVYCSCFMGSFNMYLLILMCSNVDP	292
QY	300	LIYARSOELRKTKEIICCCYPLGGLCDLSRY	332
Db	293	LIYARFSOEMRKTKFKEIVCFQGRTPCRFPSTY	325

RESULT 11

S71420
melanocortin 1 receptor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 04-Sep-1998
C;Accession: S71420
R;Takeuchi, S.; Suzuki, H.; Yabuuchi, M.; Takahashi, S.
Biochim. Biophys. Acta 1308, 164-168, 1996
A;Title: A possible involvement of melanocortin 1-receptor in regulating feather color
A;Reference number: S71420; PMID:8764834
A;Accession: S71420
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: DNA
A;Residues: 1-314 <TAK>
C;Superfamily: melanocortin receptor

RESULT 12

S70005
melanocortin 1 receptor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 15-Feb-1997 #sequence revision 27-Feb-1997 #text change 20-Jun-2000

C:Accession: S70005; S72884
R:Takeuchi, S.; Suzuki, H.; Hirose, S.; Yabuuchi, M.; Sato, C.; Yamamoto, H.; Takahashi, S.; Biochim. Biophys. Acta 1306, 122-126, 1996
A:Title: Molecular cloning and sequence analysis of the chick melanocortin 1-receptor
A:Reference number: S70005; MUID:96221280; PMID:8634326
A:Accession: S70005
A:Molecule type: DNA
A:Residues: 1-314 <TAK>
A:Cross-references: EMBL:D78272
R:Takeuchi, S.
submitted to the EMBL Data Library, November 1995
A:Reference number: S72884
A:Accession: S72884
A:Molecule type: DNA
A:Residues: 1-9, 'V', 'I', 217, 'S', 219-314 <TAW>
A:Cross-references: EMBL:D78272; NID:g1065994; PIDN:BAAL1336.1; PID:g1065995
C:Superfamily: melanocortin receptor
C:Keywords: G protein-coupled receptor; glycoprotein; lipoprotein; thiolester bond; t
F:36-61/Domain: transmembrane #status predicted <TM1>
F:71-95/Domain: transmembrane #status predicted <TM2>
F:114-138/Domain: transmembrane #status predicted <TM3>
F:162-181/Domain: transmembrane #status predicted <TM4>
F:193-209/Domain: transmembrane #status predicted <TM5>
F:237-263/Domain: transmembrane #status predicted <TM6>
F:276-297/Domain: transmembrane #status predicted <TM7>
F:15,20,23/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:312/Binding site: palmitate (Cys) (covalent) #status predicted

RESULT 13

S45708

MSH receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Dec-1994 #sequence_revision 19-Apr-1996 #text_change 20-Apr-2000
C:Accession: S45708
R:Vanetti, M.; Schoenrock, C.; Meyerhof, W.; Hoelltt, V.
FEBS Lett. 348, 268-272, 1994
A:Title: Molecular cloning of a bovine MSH receptor which is highly expressed in the
A:Reference number: S45708; MUID:94307438; PMID:8034052
A:Accession: S45708
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-317 <VAN>
A:Cross-references: GB:S71017; NID:g547325; PIDN:AAB31361.1; PID:g547326
C:Superfamily: melanocortin receptor

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 4, 2003, 18:04:01 ; Search time 14 Seconds
(without alignments)
983.581 Million cell updates/sec

Title: US-09-884-211a-4
Perfect score: 1726
Sequence: 1 MNSTLQHGHTSLHFNWRT.....FKETICCYPLGLGLDLSRY 332

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	ID	Description
1	1664	96.4	332	1	MC4R_PIG	O97504 sus scrofa
2	1638.5	94.9	332	1	MC4R_HUMAN	P32245 homo sapien
3	1628	94.3	332	1	MC4R_RAT	P70596 rattus norv
4	1590	92.1	332	1	MC4R_BOVIN	Q9qlj8 bos taurus
5	1041	60.3	325	1	MC5R_RAT	P35345 rattus norv
6	1029.5	59.6	325	1	MC5R_PANTR	Q9tt23 pan troglod
7	1026.5	59.5	325	1	MC5R_MOUSE	P41149 mus musculu
8	1025.5	59.4	325	1	MC5R_HUMAN	P33032 homo sapien
9	994	57.6	323	1	MC3R_MOUSE	P33033 mus musculu
10	982.5	56.9	360	1	MC3R_HUMAN	P41968 homo sapien
11	967.5	56.1	325	1	MC3R_BOVIN	P56451 bos taurus
12	965	55.9	323	1	MC3R_RAT	P32244 rattus norv
13	962.5	55.8	325	1	MC5R_SHEEP	P41983 ovis aries
14	941	54.5	294	1	MC5R_PIG	Q9mzv8 sus scrofa
15	928	53.8	184	1	MC4R_MOUSE	P56450 mus musculu
16	817.5	47.4	314	1	MSHR_CHICK	P55167 gallus gall
17	781.5	45.3	317	1	MSHR_CAPCA	P56443 capreolus c
18	781.5	45.3	317	1	MSHR_DAMDA	P56446 dana dama
19	777.5	45.0	317	1	MSHR_ALCA	P56442 alces alces
20	774.5	44.9	317	1	MSHR_BOVIN	P47798 bos taurus
21	770	44.6	317	1	MSHR_RANTA	P56448 rangifer ta
22	769.5	44.6	317	1	MSHR_CAPH	P56444 capra hircu
23	769.5	44.6	317	1	MSHR_CEREL	P56445 cervus elap
24	769.5	44.6	317	1	MSHR_SHEEP	P56445 ovibos mosc
25	768	44.5	317	1	MSHR_OVIMO	P56447 ovibos mosc
26	766.5	44.4	283	1	MSHR_PIG	Q9tu05 sus scrofa
27	766	44.4	317	1	MSHR_CANFA	Q97616 canis famil
28	766	44.4	317	1	MSHR_VULVU	Q29154 vulpes vulp
29	755.5	43.8	317	1	MSHR_PANTR	Q9tuk4 pan troglod
30	754.5	43.7	317	1	MSHR_HUMAN	Q01726 homo sapien
31	732.5	43.6	315	1	MSHR_MOUSE	Q01727 mus musculu
32	741.5	43.0	292	1	MSHR_HORSE	P79166 equus cabal
33	723	41.9	297	1	ACTR_HUMAN	Q01718 homo sapien

34	721	41.8	295	1	ACTR_SHEEP	Q9tu77 ovis aries
35	721	41.8	296	1	ACTR_MOUSE	Q64326 mus musculu
36	720	41.7	297	1	ACTR_BOVIN	P34974 bos taurus
37	720	41.7	297	1	ACTR_MESAU	P70115 mesocricetu
38	688	39.9	297	1	ACTR_CAVPO	Q921s9 cavia porce
39	358.5	20.8	364	1	EDG2_HUMAN	Q92633 homo sapien
40	356	20.6	364	1	EDG2_MOUSE	Q61130 mus musculu
41	348	20.2	393	1	EDG2_SHEEP	P46628 ovibos aries
42	347	20.1	364	1	EDG2_BOVIN	Q28031 bos taurus
43	346	20.0	334	1	GP12_HUMAN	P47775 homo sapien
44	337	19.5	334	1	GP12_RAT	P30951 rattus norv
45	335	19.4	334	1	GP12_MOUSE	P35412 mus musculu

ALIGNMENTS

RESULT 1						
MC4R_PIG						
ID	MC4R_PIG	STANDARD;		PRT;	332 AA.	
AC	O97504: Q9N274; Q9N141;					
DT	16-OCT-2001 (Rel. 40, Created)					
DT	16-OCT-2001 (Rel. 40, Last sequence update)					
DT	16-OCT-2001 (Rel. 40, Last annotation update)					
DE	Melanocortin-4 receptor (MC4-R).					
GN	MC4R.					
OS	Sus scrofa (Pig).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.					
OX	NCBI_TaxID=9823;					
[1]						
RP	SEQUENCE FROM N.A.					
RC	STRAIN=LMD; TISSUE=Kidney;					
RA	Ito Y., Minezawa M.;					
RL	Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.					
[2]						
RP	SEQUENCE OF 73-320 FROM N.A., AND VARIANT ASN-298.					
RX	MEDLINE=20122164; PubMed=10656927;					
RA	Kim K.S., Larsen N., Short T., Plastow G., Rothschild M.F.;					
RT	"A missense variant of the porcine melanocortin-4 receptor (MC4R) gene is associated with fatness, growth, and feed intake traits.";					
[3]						
RP	SEQUENCE OF 75-142 FROM N.A.					
RC	TISSUE=Hypothalamus;					
RA	Matteri R.L., Dyer C.J.;					
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.					
CC	FUNCTION: RECEPTOR SPECIFIC TO THE HEPTAPEPTIDE CORE COMMON TO ADRENOCORTICOTROPIC HORMONE AND ALPHA-, BETA-, AND GAMMA-MSH.					
CC	THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE CYCLASE (BY SIMILARITY).					
CC	SUBCELLULAR LOCATION: Integral membrane protein.					
CC	SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.					
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).					
DR	EMBL; AB021664; BAA36170.1;					
DR	EMBL; AF087937; AAF31753.1;					
DR	EMBL; AF227727; AAF34778.1;					
DR	InterPro; IPR000276; GPCR_Rhodpsn.					
DR	Pfam; PF00001; 7tm1.1.					
DR	PRINTS; P000237; GPCRHHODPSN.					
DR	PROSITE; PS00237; G-PROTEIN_RECF1.1; 1.					
DR	PROSITE; PS00262; G-PROTEIN_RECF1.2; 1.					
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;					
KW	Phosphorylation; Lipoprotein; Palmitate; Polymorphism.					
FT	DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).					

QY	121	IDNWIDSVICSSLLASICSLLSTAVDRYFTIFVALQYHNIMTVRRVGIISCIWAAC	TVS	180
Db	121	IDNWIDSVICSSLLASICSLLSTAVDRYFTIFVALQYHNIMTVRRVGIISCIWAAC	TVS	180
QY	181	GILFIYSDSTAVIIICLIITMFFTMLMASLYVHMFMLARLHKRIKRIAVLP	GTGTIROGAN	240
Db	181	GVLFIIYSDSSAVIIICLIITVFTTMLMASLYVHMFMLARLHKRIKRIAVLP	GTGTIROGAN	240
QY	241	MKAIAITLITLIGVYVVCWAPFFUHLFIYISCPNPYCVCFMSHFNL	YLILMCSNIIDPL	300
Db	241	MKAIAITLITLIGVYVVCWAPFFUHLFIYISCPNPYCVCFMSHFNL	YLILMCSNIIDPL	300
QY	301	IYALRSQELRKTFKEIIICVPLGGLCDLSSRY	332	
Db	301	IYALRSQELRKTFKEIIICVPLGGLCDLSSRY	332	
RESULT 5				
MC5R_RAT				
ID	MC5R_RAT	STANDARD;	PRT;	325 AA.
AC	P35345;			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	01-NOV-1995 (Rel. 32, Last annotation update)			
DE	Melanocortin-5 receptor (MC5-R).			
GN	MC5R.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
ON	NCBI_TaxID=10116;			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Striatum;			
RC	MEDLINE=94234987; PubMed=8179577;			
RA	Griffon N., Mignon V., Facchinetti P., Diaz J., Schwartz J.C.,			
RA	Sokoloff P.;			
RT	"Molecular cloning and characterization of the rat fifth melanocortin			
RT	receptor.";			
RL	Biochem. Biophys. Res. Commun. 200:1007-1014(1994).			
CC	-!- FUNCTION: RECEPTOR FOR MSH (ALPHA, BETA AND GAMMA) AND ACTH. THE			
CC	ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE			
CC	ADENYLATE CYCLASE. THIS RECEPTOR IS A POSSIBLE MEDIATOR OF THE			
CC	IMMUNOMODULATION PROPERTIES OF MELANOCORTINS.			
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-!- TISSUE SPECIFICITY: VERY LOW EXPRESSION LEVELS IS DETECTED IN			
CC	BRAIN, WHILE HIGH LEVELS ARE FOUND IN ADRENALS, STOMACH, LUNG AND			
CC	SPLEEN.			
CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL; L27081; AAA41577.1; -			
CC	PIR; JC2193; JC2193.			
DR	InterPro; IPR000276; GPCR_Rhodpsn.			
DR	Pfam; PF00001; 7tm.1; 1.			
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.			
DR	PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.			
CC	G-protein coupled receptor; Transmembrane; Glycoprotein;			
CC	Phosphorylation; Lipoprotein; Palmitate.			
CC	DOMAIN 1 37 EXTRACELLULAR (POTENTIAL).			
CC	TRANSMEM 38 61 1 (POTENTIAL)			
CC	DOMAIN 62 73 CYTOPLASMIC (POTENTIAL).			
CC	TRANSMEM 74 97 2 (POTENTIAL).			
CC	DOMAIN 98 114 EXTRACELLULAR (POTENTIAL).			
CC	TRANSMEM 115 138 3 (POTENTIAL).			
CC	DOMAIN 139 155 CYTOPLASMIC (POTENTIAL).			

30-MAY-2000 (Rel. 39, Last annotation update)
 Melanocortin-5 receptor (MC5-R).
 MC5R.
 Mus musculus (Mouse).
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 SEQUENCE FROM N.A.
 RP STRAIN=129/SV;
 RC MEDLINE=94213827; PubMed=8161509;
 RA Labbe O., Desarnaud F., Eggerickx D., Vassart G., Parmentier M.;
 RT "Molecular cloning of a mouse melanocortin 5 receptor gene widely
 expressed in peripheral tissues.";
 RL Biochemistry 33:4543-4549(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94211974; PubMed=8185570;
 RA Gantz I., Shimoto Y., Konda Y., Miwa H., Dickinson C.J., Yamada T.;
 RT "Molecular cloning, expression, and characterization of a fifth
 melanocortin receptor.";
 RL Biochem. Biophys. Res. Commun. 200:1214-1220(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95258173; PubMed=7739752;
 RA Fathi Z., Iben L.G., Parker E.M.;
 RT "Cloning, expression, and tissue distribution of a fifth melanocortin
 receptor subtype.";
 RL Neurochem. Res. 20:107-113(1995).
 CC -1- FUNCTION: RECEPTOR FOR MSH (ALPHA, BETA AND GAMMA) AND ACTH. THE
 ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
 ADENYLATE CYCLASE. THIS RECEPTOR IS A POSSIBLE MEDIATOR OF THE
 IMMUNOMODULATORY PROPERTIES OF MELANOCORTINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: SKIN, ADRENAL GLAND, SKELETAL MUSCLE,
 BONE MARROW, SPLEEN, THYMUS, GONADS, UTERUS AND BRAIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X76295; CAA53943.1; .
 DR EMBL; L22527; AAA21337.1; .
 DR EMBL; U08354; AAA76585.1; ALT_INIT.
 DR PIR; A54245; A54245.
 DR MGD; MGI:99420; Mc5r.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 37 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 38 61 1 (POTENTIAL).
 FT DOMAIN 62 73 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 74 97 2 (POTENTIAL).
 FT DOMAIN 98 114 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 115 138 3 (POTENTIAL).
 FT DOMAIN 139 155 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 156 179 4 (POTENTIAL).
 FT DOMAIN 180 186 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 187 211 5 (POTENTIAL).
 FT DOMAIN 212 239 6 (POTENTIAL).
 FT TRANSMEM 240 265 7 (POTENTIAL).
 FT DOMAIN 266 273 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 274 297 7 (POTENTIAL).
 FT DOMAIN 298 325 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 2 2 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 15 15 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT LIPID 311 311 PALMITATE (POTENTIAL).
 FT LIPID 312 312 PALMITATE (POTENTIAL).
 FT CONFLICT 74 74 F -> Y (IN REF. 2 AND 3).
 SQ SEQUENCE 325 AA; 36953 MW; 5A014D1C1E0157EE CRC64;
 Query Match 59.5%; Score 1026.5; DB 1; Length 325;
 Best Local Similarity 66.8%; Pred. No. 3:1e-62;
 Matches 195; Conservative 43; Mismatches 53; Indels 1; Gaps 1;
 QY 42 EQLFVPEVFTLGVISLLENILVIVAIAKKNLHSPMYFFICSLAVADMLSVNGSET 101
 DB 34 EENGIAVEVFTLGLVSLLENILVIGAVYKKNLHSPMYFFVGS LAVADMLSVNSAWET 93
 QY 102 IVITLNLSTD-TDAQSFVNIDNVDVSVICSSLLASICSLLSIAVDRIFFYFALQVHNI 160
 DB 94 VTYLLNNKHLVIADTFVRHIDNVFDSMICSIVVSMCSLLAIAVDRIYITFVALRYHHI 153
 QY 161 MTVRVYGIISCIAWACTVSGILFIYSDSTAVILCLITMFFTMLALMASLYVHMLMAR 220
 DB 154 MTARRSGVIIACITWTCISGIVFIYIESKYVILICLSIMFFMTLFFMVS LYIHMFLAR 213
 QY 221 LHIKRIAVLPGTGTIRQGANMKGAITITILIGVYVVCWAPFFLHLIFYISCPQNPYCVCF 280
 DB 214 NHVKRIAASPRYNSVRQRTSMKCAITLMLGLGIFVWCSPFFLHLILMISCPQNPVYCSCF 273
 QY 281 MSFNFYLLILMCSNIIDPLIYALRSQELKTKFKIICCYPLGGLCDLSRY 332
 DB 274 MSYFNMYLLIMCSVIDPLIYALRSQEMRRTFKFVCCVCHGFRPPCRLLGGY 325
 RESULT 8
 MC5R_HUMAN STANDARD; PRT; 325 AA.
 ID MC5R_HUMAN
 AC P33032;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Melanocortin-5 receptor (MC5-R) (MC-2).
 GN MC5R.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=93384614; PubMed=8396929;
 RA Chhajlani V., Muceniec R., Wikberg J.E.S.;
 RT "Molecular cloning of a novel human melanocortin receptor.";
 RL Biochem. Biophys. Res. Commun. 195:866-873(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94234987; PubMed=8179577;
 RA Griffon N., Mignon V., Facchinetti P., Diaz J., Schwartz J.C.,
 Sokoloff P.;
 RT "Molecular cloning and characterization of the rat fifth melanocortin
 receptor.";
 RL Biochem. Biophys. Res. Commun. 200:1007-1014(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=95258173; PubMed=7739752;
 RA Fathi Z., Iben L.G., Parker E.M.;
 RT "Cloning, expression, and tissue distribution of a fifth melanocortin
 receptor subtype.";
 RL Neurochem. Res. 20:107-113(1995).
 RN [4]
 RP VARIANT LEU-209.
 RX MEDLINE=21184529; PubMed=11286624;

RA Hattat N., Dixon C., Ray A.J., Phillips S.R., Cunliffe W.J., Dale M.,
 RT Todd C., Meggit S., Birch-Machin M.A., Rees J.L.;
 RT "Expression, candidate gene, and population studies of the
 RL melanocortin 5 receptor.";
 RL J. Invest. Dermatol. 116:564-570(2001).
 CC -!- FUNCTION: RECEPTOR FOR MSH (ALPHA, BETA AND GAMMA) AND ACTH. THE
 CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
 CC ADENYLATE CYCLASE. THIS RECEPTOR IS A POSSIBLE MEDIATOR OF THE
 CC IMMUNOMODULATION PROPERTIES OF MELANOCORTINS.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: IS EXPRESSED IN THE BRAIN BUT NOT IN THE
 CC MELANOMA CELLS.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; Z25470; CAA80962.1; -;
 DR EMBL; L27080; AAA59566.1; -;
 DR EMBL; U08353; AAB60376.1; -;
 DR Genew; HGNC:6933; MC5R.
 DR MIM; 600042; -;
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Phosphorylation; Lipoprotein; Palmitate; Polymorphism.
 FT DOMAIN 1 37 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 38 61 1 (POTENTIAL).
 FT DOMAIN 62 73 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 74 97 2 (POTENTIAL).
 FT DOMAIN 98 114 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 115 138 3 (POTENTIAL).
 FT DOMAIN 139 155 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 156 179 4 (POTENTIAL).
 FT DOMAIN 180 186 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 187 211 5 (POTENTIAL).
 FT DOMAIN 212 239 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 240 265 6 (POTENTIAL).
 FT DOMAIN 266 273 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 274 297 7 (POTENTIAL).
 FT DOMAIN 298 325 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 2 2 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 15 15 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT LIPID 311 311 PALMITATE (POTENTIAL).
 FT LIPID 312 312 PALMITATE (POTENTIAL).
 FT VARIANT 209 209 F -> L.
 FT CONFLICT 149 149 R -> A (IN REF. 2).
 FT CONFLICT 221 234 ALPGASARQRTSM -> LCPGPAIRGRPAW (IN
 FT REF. 1).
 FT CONFLICT 297 297 F -> Y (IN REF. 2).
 SQ SEQUENCE 325 AA; 36600 MW; 8BEC17E1BDA059BB CRC64;
 Query Match 59.4%; Score 1025.5; DB 1; Length 325;
 Best Local Similarity 62.0%; Pred. No. 3.6e-62;
 Matches 207; Conservative 43; Mismatches 71; Indels 13; Gaps 5;
 Qy 1 MNSTLQHGHTSLHFWNRSTYQGHGNAT--ESLKGYPDGGCYQLFVSPFVTLGVIS 58
 Db 1 MNSSFFH-----LHFLDLNLNATEGLSGPNVKNKSSP---C-EDMGIAVEFLTLGVIS 50
 Qy 59 LLENILVIVATKNNLHSPMYFFICSLAVADMVLSVNSGETIVTLLNSTD--TDAQSF 117
 Db 51 LLENILVIGATVKNKLNHSPMYFFVFCVSLAVADMVLSVNSAWETITVLLNKNHVLVADAF 110

Qy 118 TVNIDNVDSVICSLLASIGLSIAVDRTFTFYALQYHNIMTVRRVGIISCIWAAC 177
 Db 111 VRHIDNVFDSMICISVWASMCSSLAIAVDRTFTFYALRYHIMTARSGALIAGIWAFC 170
 Qy 178 TVSGILFTIYSDSTAVIICLTMTFTMALMASLYVHMFMLARLHKRIAVLPQTGTTRQ 237
 Db 171 TCGGVFTLYSESTYVILCLISMFAMFLVLSYIHMFLARLHKRIAVLPQTGTTRQ 230
 Qy 238 GANKMGATLITLIGVFWVWAPFLHLIFVYSCPNQYCVCFMSHFNLYLILMCNSII 297
 Db 231 RTSQMGAVTMLLGVFTVWAPFLHLTLMLSCPQNLCSRFMSHFNLYLILMCNSVM 290
 Qy 298 DPLIYALRSQELRKTFKEIICYPGLGLCLSSR 331
 Db 291 DPLIYAFRSQEMRKTFKEIICRGFRACSPRR 324
 RESULT 9
 MC3R_MOUSE STANDARD; PRT; 323 AA.
 AC P33033;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Melanocortin-3 receptor (MC3-R).
 GN MC3R.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-94226597; PubMed-8172596;
 RA Desarnaud F., Labbe O., Eggerickx D., Vassart G., Parmentier M.;
 RT "Molecular cloning, functional expression and pharmacological
 RT characterization of a mouse melanocortin receptor gene.";
 RL Biochem. J. 299:367-373(1994).
 CC -!- FUNCTION: RECEPTOR FOR MSH (ALPHA, BETA AND GAMMA) AND ACTH. THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE
 CC CYCLASE.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: BRAIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL; X74983; CAA52918.1; -;
 DR PIR; S37153; S37153.
 DR MGD; MGI:96929; Mc3r.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 37 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 38 63 1 (POTENTIAL).
 FT DOMAIN 64 75 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 76 100 2 (POTENTIAL).
 FT DOMAIN 101 118 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 119 140 3 (POTENTIAL).
 FT DOMAIN 141 160 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 161 181 4 (POTENTIAL).
 FT DOMAIN 182 186 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 187 210 5 (POTENTIAL).
 FT DOMAIN 211 245 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 246 268 6 (POTENTIAL).
 FT DOMAIN 277 301 7 (POTENTIAL).
 FT DOMAIN 302 323 7 (POTENTIAL).
 FT CARBOHYD 2 2 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT LIPID 315 315 PALMITATE (POTENTIAL).
 SQ SEQUENCE 323 AA; 35806 MW; F4B7B02FAA87B7B CRC64;

 Query Match 57.6%; Score 994; DB 1; Length 323;
 Best Local Similarity 61.7%; Pred. No. 4.6e-60;
 Matches 180; Conservative 53; Mismatches 52; Indels 8; Gaps 4;

 QY 27 ATESLQKGYDGGCYQLFVSPFVFTGLVLSLENIIVIAIAKKNLHSPMYFFICSL 86
 DB 26 ASNRSGSF---C-EQVFKPEVFLALGIVSLMENILVAVRNGNLHSPMYFFICSL 80

 QY 87 AVADMLVSVNGSETIVITLLNSTD-TDAQSFVNIDNVDVSVCSLLASISLAV 145
 DB 81 AAADMLVSLNSLETIMIAVINSLSLTLEQFIQHMNDIPDSMICISLVASICNLLAIAI 140

 QY 146 DRYFTFYALQYHINIMTVRVGIIISCIWAACVSGILEIYISDSTAVIICLITMFTML 205
 DB 141 DRVITFYAIRHSIMTVRKALTLIGVWCCGICGVWFIYSESKMIVCLITMFFAMV 200

 QY 206 ALMASLYVHMFMLARLHRIKRIAVLPGTGTI--RQGANMKGAILTILIGVYVVCWAPFFL 263
 DB 201 LLMGTYIHMFLARLHVQRIAVLPAGVVPQOHSCKMGAVITILLGVFICWAPFFL 260

 QY 264 HLIFYISCPONPCVCFMSHFNLYLILMNCNSIIDPLIYALRSQELRKFKETIC 318
 DB 261 HLVLITCTPNPCYICATYHNTFYLVLMNCNSVIDPLIYAFRSLELRNFKETIC 315

 RESULT 10
 MC3R_HUMAN STANDARD; PRT; 360 AA.
 AC P41968; Q9H517;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Melanocortin-3 receptor (MC3-R).
 GN MC3R.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93216807; PubMed=8463333;
 RA Gantz I., Konda Y., Tashiro T., Shimoto Y., Miwa H., Munzert G.,
 RA Watson S.J., Delvalle J., Yamada T.;
 RA "Molecular cloning of a novel melanocortin receptor.";
 RL J. Biol. Chem. 268:8246-8250(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Dunn N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhali P.D., Dorn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grahm D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leharvalho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,

RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
 RA .Smith C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 CC -1- FUNCTION: RECEPTOR FOR MSH (ALPHA, BETA AND GAMMA) AND ACTH. THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE
 CC CYCLASE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: BRAIN, PLACENTAL, AND GUT TISSUES.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC
 CC EMBL; L06155; AAC13541.1; -;
 CC EMBL; AL139824; CAC15480.1; -;
 CC Genew; HGNC:6931; MC3R.
 CC MIM; 155540; -;
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 74 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 75 100 1 (POTENTIAL).
 FT DOMAIN 101 112 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 113 137 2 (POTENTIAL).
 FT DOMAIN 138 155 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 156 177 3 (POTENTIAL).
 FT DOMAIN 178 197 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 198 218 4 (POTENTIAL).
 FT DOMAIN 219 223 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 224 247 5 (POTENTIAL).
 FT DOMAIN 248 282 6 (POTENTIAL).
 FT TRANSSEM 283 305 6 (POTENTIAL).
 FT DOMAIN 306 314 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 315 338 7 (POTENTIAL).
 FT DOMAIN 339 360 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT LIPID 352 352 PALMITATE (POTENTIAL).
 FT CONFLICT 6 6 T -> K (IN REF. 1).
 FT CONFLICT 81 81 V -> I (IN REF. 1).
 SQ SEQUENCE 360 AA; 40072 MW; 0D2C61195C164C51 CRC64;

 Query Match 56.9%; Score 982.5; DB 1; Length 360;
 Best Local Similarity 64.3%; Pred. No. 3e-59;
 Matches 180; Conservative 49; Mismatches 48; Indels 3; Gaps 2;

 QY 42 EQLFVSPFVFTGLVSVISLENIIVIAIAKKNLHSPMYFFICSLAVADMLVSVNGSET 101
 DB 73 EQVFKPEVFLSLGIVLSLENIIVIAIAKKNLHSPMYFFICSLAVADMLVSVNGSET 132

 QY 102 IVITILNSPD-TDAQSFVNIDNVDVSVCSLLASISLAVDRYFTIFVALQYHNI 160
 DB 133 IMIAVHSYLTFFEDQFIQHMNDIPDSMICISLVASICNLLAIAVDRYFTIFVALYHNI 192

 QY 161 MTVRVRGIIISCIWAACVSGILEIYISDSTAVIICLITMFTMLMASLYVHMFMLMAR 220


```
RESULT 14
MC5R_PIG
ID MC5R_PIG STANDARD; PRT; 294 AA.
AC 09NZV8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melanocortin-5 receptor (Fragment).
GN MC5R.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20353873; PubMed=10895318;
RA Kim K.S., Marklund S., Rothschild M.F.;
RT "The proline melanocortin-5 receptor (MC5R) gene: polymorphisms,
linkage and physical mapping.";
RL Anlm. Genet. 31:230-231(2000).
CC -!- FUNCTION: RECEPTOR FOR MSH (ALPHA, BETA AND GAMMA) AND ACTH. THE
ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
ADENYLATE CYCLASE. THIS RECEPTOR IS A POSSIBLE MEDIATOR OF THE
IMMUNOMODULATION PROPERTIES OF MELANOCORTINS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; AF133793; AAF82610.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT NON_TER 1 1
FT DOMAIN <1 29 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 30 53 1 (POTENTIAL).
FT DOMAIN 54 65 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 66 89 2 (POTENTIAL).
FT DOMAIN 90 106 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 107 130 3 (POTENTIAL).
FT DOMAIN 131 147 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 148 171 4 (POTENTIAL).
FT DOMAIN 172 178 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 179 203 5 (POTENTIAL).
FT DOMAIN 204 231 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 232 257 6 (POTENTIAL).
FT DOMAIN 258 265 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 266 289 7 (POTENTIAL).
FT DOMAIN 290 >294 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 7 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 12 12 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 20 20 N-LINKED (GLCNAC. .) (POTENTIAL).
FT NON_TER 294 294
SQ SEQUENCE 294 AA; 32753 MW; C6ED78FA26B55D42 CRC64;

Query Match 54.5%; Score 941; DB 1; Length 294;
Best Local Similarity 64.0%; Pred. No. 1.5e-56;
Matches 187; Conservative 38; Mismatches 53; Indels 14; Gaps 4;

QY 26 NATESLCKGYPDGG----CYEQLFVSPVEFVTLGLVLSILENLIIVAIKKNKLNHSPMYF 81
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
7 NATEGNVSGPSVGNSSPC-EDMGIEVEFVTLGLVLSILENLIIVAIKKNKLNHSPMYF 65
82 FICSLAVADMVLSVNSNGSETIVITLLNS-----TDTDAQSFVTNIDNVIDSVICSSLLAS 136

RESULT 15
MC4R_MOUSE
ID MC4R_MOUSE STANDARD; PRT; 184 AA.
AC P56450;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Melanocortin-4 receptor (MC4-R) (Fragment).
GN MC4R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ICR; TISSUE=Anterior pituitary;
RA Morooka Y., Oomizu S., Takeuchi S., Takahashi S.;
RL Submitted (DSC-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR SPECIFIC TO THE HEPTAPEPTIDE CORE COMMON TO
ADRENOCORTICOTROPIC HORMONE AND ALPHA-, BETA-, AND GAMMA-MSH.
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE
CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
CC EMBL; AB009664; BAA24015.1; -.
DR MGD; MGI:99457; MC4r.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
Phosphorylation; Lipoprotein; Palmitate.
FT NON_TER 1 1
FT DOMAIN <1 12 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 13 34 3 (POTENTIAL).
FT DOMAIN 35 54 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 55 75 4 (POTENTIAL).
FT DOMAIN 76 80 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 81 104 5 (POTENTIAL).
FT DOMAIN 105 137 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 138 160 6 (POTENTIAL).
FT DOMAIN 161 169 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 170 >184 7 (POTENTIAL).
FT NON_TER 184 184
SQ SEQUENCE 184 AA; 20614 MW; 9C61CAD31BA0DE33 CRC64;

Query Match 53.8%; Score 928; DB 1; Length 184;
Best Local Similarity 95.7%; Pred. No. 7.3e-56;
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Matches	176;	Conservative	6;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	112	TDQSFVNIDNVIDSVICSSLLASICSLSIAVDRYFTIFYALQYHNIMTVRRVGIIIS	171						
Db	1	TDQSFVNIDNVIDSVICSSLLASICSLSIAVDRYFTIFYALQYHNIMTVRRVGIIIS	60						
Qy	172	CIWAACVSGILFIYSDSTAVIICLTMEFTMLALMASLYVHMFELMARLHKRIAVLPG	231						
Db	61	CIWAACVSGVLFYIYSDSSAVIICLTISMFTMLVLMASLYVHMFELMARLHKRIAVLPG	120						
Qy	232	TGTIROGANNKGATITLILIGVFVVCWAPFELHLIFYISCPQNPYCVCFMSHENLYLILI	291						
Db	121	TGTIROGTNNKGATITLILIGVFVVCWAPFELHLIFYISCPQNPYCVCFMSHENLYLILM	180						
Qy	292	MCNS	295						
Db	181	MCNA	184						

Search completed: June 4, 2003, 18:16:18
 Job time : 15 secs

Result No.	Query	Score			DB	ID	Description
		Match	Length				
1	1636	94.8	332	11	Q9E0M7	Q9eqm7 mus musculus	
2	1490.5	86.4	331	13	Q73667	Q73667 gallus gall	
3	1162.5	67.4	322	13	Q90X73	Q90y73 takifugu po	
4	1162.5	67.4	322	13	Q90YV0	Q90yV0 takifugu ch	
5	1157.5	67.1	322	13	Q90X74	Q90y74 takifugu ra	
6	1157.5	67.1	322	13	Q90X72	Q90y72 takifugu po	
7	1115.5	64.6	325	13	Q73671	Q73671 gallus gall	
8	1099	63.7	223	6	Q95LB5	Q95lb5 ovis aries	
9	1025.5	59.4	325	13	Q93Z59	Q93z59 gallus gall	
10	823	47.7	314	13	Q90ZP7	Q90zp7 tangara cuc	
11	822	47.6	314	13	Q90YV8	Q90yV8 coereba fla	
12	821	47.6	314	13	Q90ZQ0	Q90zQ0 coereba fla	
13	821	47.6	314	13	Q90VX9	Q90vX9 coereba fla	
14	818	47.4	314	13	Q90ZP8	Q90zp8 coereba fla	
15	818	47.4	314	13	Q90YV8	Q90yV8 coereba fla	
16	816	47.3	314	13	Q90ZP9	Q90zp9 coereba fla	

```
QY 61 ENILVVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDDAQSFTVN 120
Db 61 ENILVVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDDAQSFTVN 120
QY 121 IDNVDSVICSLLASICSLLSTAVDRYETIFALQYHNMVRRVGGIISCIWAACVTS 180
Db 121 IDNVDSVICSLLASICSLLSTAVDRYETIFALQYHNMVRRVGGIISCIWAACVTS 180
QY 181 GILFIYSDSTAVIICLTIMFTMLMASLVVHMFMLARLHKRIAVLPGTGTROGAN 240
Db 181 GILFIYSDSTAVIICLTIMFTMLMASLVVHMFMLARLHKRIAVLPGTGTROGAN 240
QY 241 MGKAITLTILIGVVFVWAPFFLHLFIYISCPNPYCVCFMSHFNLYLILMNCNIIIDPL 300
Db 241 MGKAITLTILIGVVFVWAPFFLHLFIYISCPNPYCVCFMSHFNLYLILMNCNIIIDPL 300
QY 301 IYALRSQELRKTFKEIICYPGLGGLDLSRY 332
Db 301 IYALRSQELRKTFKEIICYPGLGGLDLSRY 332
RESULT 2
O73667 PRELIMINARY; PRT; 331 AA.
AC O73667;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Melanocortin 4-receptor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGHONE; TISSUE=LIVER;
RA Takeuchi S., Takahashi S.;
RT "Molecular cloning of the chicken melanocortin 4-receptor gene widely
expressed in peripheral tissues.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AB012211; BAA25252.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 331 AA; 36984 MW; 98B25F5A1FFB02C1 CRC64;
Query Match 86.4%; Score 1490.5; DB 13; Length 331;
Best Local Similarity 86.4%; Pred. No. 1.9e-123;
Matches 287; Conservative 16; Mismatches 28; Indels 1; Gaps 1;
QY 1 MNSTLQHGHTSLHFNWSTYQHGNGATESLGKYPDGGCYEQLFVSPFVTLGLVISLL 60
Db 1 MNFTQHRGTLOPLHFNQSN-GLHRGASEPSAKHSGCYEQLFVSPFVTLGLISLL 59
QY 61 ENILVVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDDAQSFTVN 120
Db 60 ENVLVVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDDAQSFTVN 119
QY 121 IDNVDSVICSLLASICSLLSIADRYETIFALQYHNMVRRVGGIISCIWAACVTS 180
Db 120 IDNVDSVICSLLASICSLLSIADRYETIFALQYHNMVRRVGGIISCIWAACVTS 179
QY 181 GILFIYSDSTAVIICLTIMFTMLMASLVVHMFMLARLHKRIAVLPGTGTROGAN 240
Db 180 GILFIYSDSSVVIICLISMEFTMLILMASLVVHMFMMARHKRIAVLPGTGTROGAN 239
QY 241 MGKAITLTILIGVVFVWAPFFLHLFIYISCPNPYCVCFMSHFNLYLILMNCNIIIDPL 300
Db 241 MGKAITLTILIGVVFVWAPFFLHLFIYISCPNPYCVCFMSHFNLYLILMNCNIIIDPL 300
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Db 240 MGKAITLTILIGVVFVWAPFFLHLFIYISCPNPYCVCFMSHFNLYLILMNCNIIIDPL 299
QY 301 IYALRSQELRKTFKEIICYPGLGGLDLSRY 332
Db 300 IYAFRSQELRKTFKEIICCCNLRGLCDLPKY 331
RESULT 3
O90Y73 PRELIMINARY; PRT; 322 AA.
AC O90Y73;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Melanocortin receptor-1.
GN MCLR.
OS Takifugu porphyreus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=176187;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunimoto M., Mizukami Y.;
RT "Discrimination of Takifugu species based on melanocortin receptor-1
gene nucleotide sequence.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073677; BAB17133.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35948 MW; A16712C763F91236 CRC64;
Query Match 67.4%; Score 1162.5; DB 13; Length 322;
Best Local Similarity 77.0%; Pred. No. 1.5e-94;
Matches 217; Conservative 31; Mismatches 33; Indels 1; Gaps 1;
QY 39 GCYEQLFVSPFVTLGVISLLENILVIVATAKKNLHSPMYFFICSLAVADMLVSVNSG 98
Db 34 GCYEQLMISLTVFLTGIIISLLENILVVAIVKKNLHSPMYFFICSLAVADMLVSVNSA 93
QY 99 SETIVITLLNS-TDTDAQSFVNIDNVIDSVICSSLLASICSLLSTAVDRYETIFALQY 157
Db 94 SETIVIALNSGTLTIPATLIKSDNVDSCSSLLASICSLLAIVDRYETIFALRY 153
QY 158 HNIMTVRRVGGIISCIWAACVSGILFIYSDSTAVIICLTIMFTMLMASLVVHMF 217
Db 154 HNIVTLRRASLVISSTCTVSGVLFIVYSESTVLICLTIMFTMLMASLVVHMF 213
QY 218 MARLHKRIAVLPGTGTROGANMKGATLTILIGVVFVWAPFFLHLFIYISCPNPY 277
Db 214 LARLHKRIAMPGNAPLHROANLKGATLTILIGVVFVWAPFFLHLITMTCPKNPY 273
QY 278 VCFMSHFNLYLILMNCNIIIDPLIYALRSQELRKTFKEIIC 319
Db 274 TCFMSHFNLYLILMNCNIIIDPLIYAFRSQEMRKTFKEIICC 315
RESULT 4
O90YVO PRELIMINARY; PRT; 322 AA.
AC O90YVO;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Melanocortin receptor-1.
GN MCLR.
OS Takifugu chinensis, and
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=176185, 31033;
EN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=T.chinensis, and F.rubripes;
RA Kunimoto M., Mizukami Y.;
RA "Discrimination of Takifugu species based on melanocortin receptor-1
RT gene nucleotide sequence.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073675; BAB71731.1; -.
DR EMBL; AB073674; BAB71730.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1.1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35975 MW; 8AF03A6371F5E1F6 CRC64;

Query Match 67.4%; Score 1162.5; DB 13; Length 322;
Best Local Similarity 77.0%; Pred. No. 1.5e-94;
Matches 217; Conservative 31; Mismatches 33; Indels 1; Gaps 1;

Oy 39 GCYEQLFVSPVFTLVGLVISLLENILVIAIAKKNLHSPMYFFICSIAVADMLVSVSNG 98
Db 34 GCYEQMLISTEVFTLVGLISLLENILVAAIVKKNLHSPMYFFICSIAVADMLVSVNA 93

Oy 99 SETIVILLNS-TDTDAQSTFVNIDNVDVSDVAVIICLTMTFETMLALMASLYVHMFL 217
Db 94 SETIVIALNSGTLTIPATLIKSDNVDVSDVAVIICLTMTFETMLALMASLYVHMFL 213

Oy 158 HNIMTVRRVGIISCIWAACVSGILFTIYSDTAVIICLTMTFETMLALMASLYVHMFL 217
Db 154 HNIVTLRRASLVSIISWTCTVSGVLFIVYSESTVLICLTMTFETMLALMASLYVHMFL 213

Oy 218 MARLHKIRIAVLPCTGTIRQGANMKGATITLIGVFVVCWAPFFLHLIFVISCQPNPYC 277
Db 214 LARLHMKRIAAMPGNAPHQRANLKGATITLIGVFVVCWAPFFLHLILMITCPKNPYC 273

Oy 278 VCFMSHNLYLILMCSNIDPLIYALRSQELRTFKEIICC 319
Db 274 TCFMSHFNMYLILMCSNIDPIIYAFRSQEMRKTEIFECC 315

RESULT 5
Q90Y74 PRELIMINARY; PRT; 322 AA.
AC Q90Y74;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Melanocortin receptor-1.
GN MC1R.
OS Takifugu poecilonotus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=176185;
EN [1]
RP SEQUENCE FROM N.A.
RA Kunimoto M., Mizukami Y.;
RA "Discrimination of Takifugu species based on melanocortin receptor-1
RT gene nucleotide sequence.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073678; BAB71734.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1.1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35945 MW; 1C3F1B3BCED4BFF8 CRC64;

Query Match 67.1%; Score 1157.5; DB 13; Length 322;
Best Local Similarity 76.6%; Pred. No. 4.1e-94;
Matches 216; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

Oy 39 GCYEQLFVSPVFTLVGLVISLLENILVIAIAKKNLHSPMYFFICSIAVADMLVSVSNG 98
Db 34 GCYEQMLISTEVFTLVGLISLLENILVAAIVKKNLHSPMYFFICSIAVADMLVSVNA 93

Oy 99 SETIVILLNS-TDTDAQSTFVNIDNVDVSDVAVIICLTMTFETMLALMASLYVHMFL 217
Db 94 SETIVIALNSGTLTIPATLIKSDNVDVSDVAVIICLTMTFETMLALMASLYVHMFL 213

Oy 158 HNIMTVRRVGIISCIWAACVSGILFTIYSDTAVIICLTMTFETMLALMASLYVHMFL 217
Db 154 HNIVTLRRASLVSIISWTCTVSGVLFIVYSESTVLICLTMTFETMLALMASLYVHMFL 213

Oy 218 MARLHKIRIAVLPCTGTIRQGANMKGATITLIGVFVVCWAPFFLHLIFVISCQPNPYC 277
Db 214 LARLHMKRIAAMPGNAPHQRANLKGATITLIGVFVVCWAPFFLHLILMITCPKNPYC 273

Oy 278 VCFMSHNLYLILMCSNIDPLIYALRSQELRTFKEIICC 319
Db 274 TCFMSHFNMYLILMCSNIDPIIYAFRSQEMRKTEIFECC 315

RESULT 5
Q90Y74 PRELIMINARY; PRT; 322 AA.
AC Q90Y74;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Melanocortin receptor-1.
GN MC1R.
OS Takifugu radiatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=176186;
EN [1]
RP SEQUENCE FROM N.A.
RA Kunimoto M., Mizukami Y.;
RA "Discrimination of Takifugu species based on melanocortin receptor-1
RT gene nucleotide sequence.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073676; BAB71732.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1.1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35917 MW; 37A8339FDCD84C38 CRC64;

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Query Match 67.1%; Score 1157.5; DB 13; Length 322;
Best Local Similarity 76.6%; Pred. No. 4.1e-94;
Matches 216; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

Oy 39 GCYEQLFVSPVFTLVGLVISLLENILVIAIAKKNLHSPMYFFICSIAVADMLVSVSNG 98
Db 34 GCYEQMLISTEVFTLVGLISLLENILVAAIVKKNLHSPMYFFICSIAVADMLVSVNA 93

Oy 99 SETIVILLNS-TDTDAQSTFVNIDNVDVSDVAVIICLTMTFETMLALMASLYVHMFL 217
Db 94 SETIVIALNSGTLTIPATLIKSDNVDVSDVAVIICLTMTFETMLALMASLYVHMFL 213

Oy 158 HNIMTVRRVGIISCIWAACVSGILFTIYSDTAVIICLTMTFETMLALMASLYVHMFL 217
Db 154 HNIVTLRRASLVSIISWTCTVSGVLFIVYSESTVLICLTMTFETMLALMASLYVHMFL 213

Oy 218 MARLHKIRIAVLPCTGTIRQGANMKGATITLIGVFVVCWAPFFLHLIFVISCQPNPYC 277
Db 214 LARLHMKRIAAMPGNAPHQRANLKGATITLIGVFVVCWAPFFLHLILMITCPKNPYC 273

Oy 278 VCFMSHNLYLILMCSNIDPLIYALRSQELRTFKEIICC 319
Db 274 TCFMSHFNMYLILMCSNIDPIIYAFRSQEMRKTEIFECC 315

RESULT 6
Q90Y72 PRELIMINARY; PRT; 322 AA.
AC Q90Y72;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Melanocortin receptor-1.
GN MC1R.
OS Takifugu poecilonotus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=176188;
EN [1]
RP SEQUENCE FROM N.A.
RA Kunimoto M., Mizukami Y.;
RA "Discrimination of Takifugu species based on melanocortin receptor-1
RT gene nucleotide sequence.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073678; BAB71734.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1.1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35945 MW; 1C3F1B3BCED4BFF8 CRC64;

Query Match 67.1%; Score 1157.5; DB 13; Length 322;
Best Local Similarity 76.6%; Pred. No. 4.1e-94;
Matches 216; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

Oy 39 GCYEQLFVSPVFTLVGLVISLLENILVIAIAKKNLHSPMYFFICSIAVADMLVSVSNG 98
Db 34 GCYEQMLISTEVFTLVGLISLLENILVAAIVKKNLHSPMYFFICSIAVADMLVSVNA 93

Oy 99 SETIVILLNS-TDTDAQSTFVNIDNVDVSDVAVIICLTMTFETMLALMASLYVHMFL 217
Db 94 SETIVIALNSGTLTIPATLIKSDNVDVSDVAVIICLTMTFETMLALMASLYVHMFL 213

Oy 158 HNIMTVRRVGIISCIWAACVSGILFTIYSDTAVIICLTMTFETMLALMASLYVHMFL 217
Db 154 HNIVTLRRASLVSIISWTCTVSGVLFIVYSESTVLICLTMTFETMLALMASLYVHMFL 213

Oy 218 MARLHKIRIAVLPCTGTIRQGANMKGATITLIGVFVVCWAPFFLHLIFVISCQPNPYC 277
Db 214 LARLHMKRIAAMPGNAPHQRANLKGATITLIGVFVVCWAPFFLHLILMITCPKNPYC 277

Oy 278 VCFMSHNLYLILMCSNIDPLIYALRSQELRTFKEIICC 319
Db 274 TCFMSHFNMYLILMCSNIDPIIYAFRSQEMRKTEIFECC 315

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Db 214 LARLHMKRIAMPONAPIHQORANLKGAITLTLLGVVFWVCWAPFFLLHLLMITCPKNPYC 273
Qy 278 VCFMSHFNLYLILIMCNSIIDPLIYALRSQELRKFKEIICC 319
Db 274 TCFMSHFNMYLILIMCNSVIDPIIYAFRSQEMRKTKEIFCC 315

RESULT 7
073671
ID 073671 PRELIMINARY; PRT; 325 AA.
AC 073671;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Melanocortin 5-receptor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LEGHONE; TISSUE=LIVER;
RA Takeuchi S., Takahashi S.;
RT "Cloning and expression of the chicken melanocortin 5-receptor gene.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB012868; BAA25640.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 325 AA; 36994 MW; 35441907C71E4FA2 CRC64;

Query Match 64.6%; Score 1115.5; DB 13; Length 325;
Best Local Similarity 65.3%; Pred. No. 21e-90;
Matches 215; Conservative 46; Mismatches 59; Indels 9; Gaps 4;

Qy 9 MHTSLFW----NRSTYGHGNATESLKGYPDGGCYEQLFVPEVFTLGVLSLLENIL 64
Db 1 MNTSSQLYSELNLSAFSGNFTVPTVKSSP---C-EQVVIAAEVFLILGIVSLLENIL 56
Qy 65 VIVAIKNNLHSPMVFYFSCSLAVADMLVSVNGSETIVITLNSDTDAQ-SFTVNIDN 123
Db 57 VICAIKNNLHSPMVFYFSCSLAVADMLVSVNSAWETITITILNNRHIIIMEDAFVRHIDN 116
Qy 124 VIDSVICSSILASICSLLSTAVDRYFTIFVALQYHNIMTVRRVGIISCIWAACVTSVSGIL 183
Db 117 VFDSLICISVWAMCSLLAIVDRYITIFVALRYHNIMTVKRSGLLIACIWTFCGCGII 176
Qy 184 FIYSDSTAVIICLTIMFTMLMALMASLYVHMFMLARLHKRIAVLPCTGTIROGANNMKG 243
Db 177 FIIYESTVVIICLTIMFTMLFLMVSIVHMFLLARTHVKKIAALPGYNSVHQRTSMKG 236
Qy 244 AITLTILGVVVCWAPFFLHLFIYISCPNQPYCVCFMSHFNLYLILIMCNSIIDPLIYA 303
Db 237 AITLTMLLGIYVWAPFFLHLFIYISCPNQLYCVCFMSHFNLYLILIMCNSVIDPLIYA 296
Qy 304 LRSQELRKFKEIICYPGLGGLDLSRY 332
Db 297 FRSQENRKFKEIICYSVRMVGGLSNKY 325

RESULT 8
Q95LB5
ID Q95LB5 PRELIMINARY; PRT; 223 AA.
AC Q95LB5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Melanocortin-4 receptor (Fragment).
GN MC4-R.
OS Ovis aries (Sheep).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21421436; PubMed=11530231;
RA Iqbal J., Pompolo S., Dumont L.M., Wu C., Mountjoy K.G., Henry B.A.,
RA Clarke I.J.;
RT "Long-term alterations in body weight do not affect the expression of
RT melanocortin receptor-3 and -4 mRNA in the ovine hypothalamus.";
RL Neuroscience 105:931-940(2001).
DR EMBL; AF345913; AAL27186.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
KW NON_TER 1
FT NON_TER 223
FT NON_TER 223
SQ SEQUENCE 223 AA; 24542 MW; C8EBB5EBCAB766E CRC64;

Query Match 63.7%; Score 1099; DB 6; Length 223;
Best Local Similarity 96.0%; Pred. No. 4e-89;
Matches 214; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 82 FICSLAVADMLVSVNGSETIVITLNSDTDAQSFVNIDNVDSVCSLLASICSLL 141
Db 1 FICSLAVADMLVSVNGSETIVITLNSDTDAQSFVNIDNVDSVCSLLASICSLL 60
Qy 142 STAVDRYFTIFVALQYHNIMTVRRVGIISCIWAACVTSVSGILFIYSDSTAVIICLTIMF 201
Db 61 STAVDRYFTIFVALQYHSINTYRVVAITISAIWAACVTSVSGVFIYSDSSAVIICLTITVF 120
Qy 202 FTMLMALASLYVHMFMLARLHKRIAVLPCTGTIROGANNMKGAITITILIGVFVVCWAPF 261
Db 121 FTMLMALASLYVHMFMLARLHKRIAVLPCTGTIROGANNMKGAITITILIGVFVVCWAPF 180
Qy 262 FLHLFIYISCPNQPYCVCFMSHFNLYLILIMCNSIIDPLIYAL 304
Db 181 FLHLFIYISCPNQPYCVCFMSHFNLYLILIMCNSVIDPLIYAL 223

RESULT 9
093259
ID 093259 PRELIMINARY; PRT; 325 AA.
AC 093259;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Melanocortin 3-receptor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LEGHORN;
RX MEDLINE=99144114; PubMed=9990303;
RA Takeuchi S., Takahashi S.;
RT "A possible involvement of melanocortin 3-receptor in the regulation
RT of adrenal gland function in the chicken.";
RL Biochim. Biophys. Acta 1448:512-518(1999).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AB017137; BAA32555.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_FL_2; 1.
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KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
 SQ SEQUENCE 325 AA; 36501 MW; 94FA6631ED144C17 CRC64;

Query Match 59.4%; Score 1025.5; DB 13; Length 325;
 Best Local Similarity 66.0%; Pred. No. 1.8e-82;
 Matches 200; Conservative 35; Mismatches 55; Indels 13; Gaps 4;

Qy 26 NATES-----LGKGPDPGCGCYEQLFVSPVEFVTLGVISLLENILVIVAIAKNKLNHSPMY 80
 Db 16 NVTEIDISILNRRSSDGFCEQVFIKAIEFLTLGIISLLENILVILAVALKNGNLSHPMY 74
 Qy 81 FFICSLAVADMLVSVNGSEFIVITLLNS-----TDTDAQSFVNIDNVDSVICSLLAS 136
 Db 75 FFLCSLAVADMLVSTNALETIMAILSSGYLIID---DHFIQHMDNVFDSMICISLAS 131
 Qy 137 ICSLLSIAVDRYFTIFVALQVHNMTVRRVGIISCIWAACVSGILFIYSDSTAVIIC 196
 Db 132 ICNLUVAIDRYITIFVALYHNTVYKKTALTLVLWISCIIGCIIFIAYSKSTVIVC 191
 Qy 197 LITMFFTMLALMASLYVHMFMLARLHKRIKRIAVLPGTGTIROGANNKGAITLTILIGVFV 256
 Db 192 LITMFFTMLFALMASLYVHMFELARLHKRIKRIALPVDGVPSTCKGAIITLTILIGVFIV 251
 Qy 257 CWAPFFLHLIFYISCPNPYCVCFMSHFNLYLILMCNSIIDPLIYALRSOELRKTKEI 316
 Db 252 CWAPFFLHLILIISCPNPYCVCTSHFTVYLVLMCMNSVIDPLIYAFRSELMRKTKEI 311
 Qy 317 ICC 319
 Db 312 VCC 314

RESULT 10
 Q902P7 PRELIMINARY; PRT; 314 AA.

ID Q902P7
 AC Q902P7
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Melanocortin 1 receptor.
 OS Tangara cucullata.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Passeriformes; Passeroidea;
 OC Fringillidae; Emberizinae; Tangara.
 OX NCBI_taxID=158457;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21261843; PubMed=11369199;
 RA Theron E., Hawkins K., Bermingham E., Ricklefs R.E., Mundy N.I.;
 RT "The molecular basis of an avian plumage polymorphism in the wild: a
 melanocortin-1-receptor point mutation is perfectly associated with
 the melanic plumage morph of the bananaquit, Coereba flaveola.";
 RL Curr. Biol. 11:550-557(2001).
 DR EMBL; AF362600; AAK50807.1;
 DR EMBL; AF362575; AAK50782.1;
 DR EMBL; AF362576; AAK50783.1;
 DR EMBL; AF362577; AAK50784.1;
 DR EMBL; AF362579; AAK50786.1;
 DR EMBL; AF362580; AAK50787.1;
 DR EMBL; AF362581; AAK50788.1;
 DR EMBL; AF362582; AAK50789.1;
 DR EMBL; AF362585; AAK50792.1;
 DR EMBL; AF362587; AAK50794.1;
 DR EMBL; AF362588; AAK50795.1;
 DR EMBL; AF362589; AAK50796.1;
 DR EMBL; AF362590; AAK50797.1;
 DR EMBL; AF362591; AAK50798.1;
 DR EMBL; AF362592; AAK50799.1;
 DR EMBL; AF362593; AAK50800.1;
 DR EMBL; AF362594; AAK50801.1;
 DR EMBL; AF362595; AAK50802.1;
 DR EMBL; AF362596; AAK50803.1;
 DR EMBL; AF362597; AAK50804.1;
 DR EMBL; AF362598; AAK50805.1;
 DR EMBL; AF362599; AAK50806.1;
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1.1.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
 DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 314 AA; 35015 MW; ACB246930C38DD89 CRC64;

Query Match 47.7%; Score 823; DB 13; Length 314;
 Best Local Similarity 51.0%; Pred. No. 1.2e-64;
 Matches 155; Conservative 60; Mismatches 83; Indels 6; Gaps 2;

Qy 17 NRSTYGQHGHNATESLGRKYPDGGCYEQLFVSPVEFVTLGVISLLENILVIVAIAKNKLNH 76
 Db 14 SNASEGHNHSTNATGAGGWCQ-----LDIPSELFALGLVSLVENLLVVAAILKRNH 68
 Qy 77 SPMTFFICSLAVADMLVSVNGSEFIVITLL-NTDITDAQSFVNIDNVDSVICSLLA 135
 Db 69 SPTYFICCLAVSDMLVSIISLAEMFLMLLLEHGLVVMRPSIVRHMDSVIDTLTICSSVFS 128

Qy 136 SICSLLSIAVDRYFTIFVALQVHNMTVRRVGIISCIWAACVSGILFIYSDSTAVII 195
 Db 129 SLSLGLVAVDRYITIFVALRYHSTMTLQRAVTVMASVWLASTVSSTVLIAYRSNTVLL 188
 Qy 196 CLITMFFTMLALMASLYVHMFMLARLHKRIKRIAVLPGTGTIROGANNKGAITLTILIGVFV 255
 Db 189 CLIGFFFLMLVLMVLVYHMFALARHHLHSISSQOKPPTAHRGGSLKGAVALTTLIGVFF 248
 Qy 256 VCWAPFFLHLIFYISCPNPYCVCFMSHFNLYLILMCNSIIDPLIYALRSOELRKTKE 315
 Db 249 ICWGPFFHLLIVTCTNPFTCFYSFNLFLILICNSVIDPLIYAFRSEQLRRTLRE 308
 Qy 316 IICC 319
 Db 309 VVTC 312

RESULT 11
 Q90VV8 PRELIMINARY; PRT; 314 AA.

ID Q90VV8
 AC Q90VV8
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Melanocortin 1 receptor.
 OS Coereba flaveola (bananaquit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Passeriformes; Passeroidea;
 OC Fringillidae; Emberizinae; Coereba.
 OX NCBI_taxID=87177;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21261843; PubMed=11369199;
 RA Theron E., Hawkins K., Bermingham E., Ricklefs R.E., Mundy N.I.;
 RT "The molecular basis of an avian plumage polymorphism in the wild: a
 melanocortin-1-receptor point mutation is perfectly associated with
 the melanic plumage morph of the bananaquit, Coereba flaveola.";
 RL Curr. Biol. 11:550-557(2001).
 DR EMBL; AF362600; AAK50807.1;
 DR EMBL; AF362575; AAK50782.1;
 DR EMBL; AF362576; AAK50783.1;
 DR EMBL; AF362577; AAK50784.1;
 DR EMBL; AF362579; AAK50786.1;
 DR EMBL; AF362580; AAK50787.1;
 DR EMBL; AF362581; AAK50788.1;
 DR EMBL; AF362582; AAK50789.1;
 DR EMBL; AF362585; AAK50792.1;
 DR EMBL; AF362587; AAK50794.1;
 DR EMBL; AF362588; AAK50795.1;
 DR EMBL; AF362589; AAK50796.1;
 DR EMBL; AF362590; AAK50797.1;
 DR EMBL; AF362591; AAK50798.1;
 DR EMBL; AF362592; AAK50799.1;
 DR EMBL; AF362593; AAK50800.1;
 DR EMBL; AF362594; AAK50801.1;
 DR EMBL; AF362595; AAK50802.1;
 DR EMBL; AF362596; AAK50803.1;
 DR EMBL; AF362597; AAK50804.1;
 DR EMBL; AF362598; AAK50805.1;
 DR EMBL; AF362599; AAK50806.1;
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1.1.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
 DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 314 AA; 35008 MW; CB704F205AB3C556 CRC64;

Query Match 47.6%; Score 822; DB 13; Length 314;
 Best Local Similarity 50.7%; Pred. No. 1.5e-64;
 Matches 154; Conservative 62; Mismatches 82; Indels 6; Gaps 2;

Qy 17 NRSTYGQHGHNATESLGRKYPDGGCYEQLFVSPVEFVTLGVISLLENILVIVAIAKNKLNH 76
 Db 14 SNASEGHNHSTNATGAGGWCQ-----LDIPSELFALGLVSLVENLLVVAAILKRNH 68
 Qy 77 SPMTFFICSLAVADMLVSVNGSEFIVITLL-NTDITDAQSFVNIDNVDSVICSLLA 135
 Db 69 SPTYFICCLAVSDMLVSIISLAEMFLMLLLEHGLVVMRPSIVRHMDSVIDTLTICSSVFS 128

[illegible]

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OM nucleic - nucleic search, using sw model

Run on: June 14, 2003, 10:15:58 ; Search time 76 Seconds
(without alignments)
8009.913 Million cell updates/sec

Title: US-09-884-211a-2

Perfect score: 1985

Sequence: 1 ctaagaccgtggggagcgag.....gaaataaaaaaaaaaaaaa 1985

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	958.2	48.3	1671	2	US-08-662-560-1
2	958.2	48.3	1671	2	US-08-780-749A-5
3	958.2	48.3	1671	4	US-08-870-511-5
4	939	47.3	1671	3	US-08-706-281A-15
5	939	47.3	1671	4	US-09-097-231-15
6	817.4	41.2	996	1	US-08-671-525B-7
7	817.4	41.2	996	1	US-08-672-109B-7
8	817.4	41.2	996	1	US-08-842-045-7
9	817.4	41.2	996	2	US-08-842-238-7
10	817.4	41.2	996	3	US-08-629-335B-7
11	815.6	41.1	999	4	US-08-870-511-7
12	815.6	41.1	999	4	US-08-870-511-9
13	815.6	41.1	999	4	US-08-870-511-11
14	436.2	21.5	975	1	US-08-671-525B-9
15	426.2	21.5	975	1	US-08-672-109B-9
16	426.2	21.5	975	1	US-08-842-045-9
17	426.2	21.5	975	2	US-08-842-238-9
18	426.2	21.5	975	3	US-08-629-335B-9
19	426	21.5	978	3	US-08-706-281A-17
20	424.8	21.4	1650	4	US-09-097-231-17
21	424.8	21.4	1650	4	US-08-387-805-15
22	396.6	20.0	1080	1	US-08-671-525B-5
23	396.6	20.0	1080	1	US-08-672-109B-5
24	396.6	20.0	1080	1	US-08-842-045-5
25	396.6	20.0	1080	2	US-08-842-238-5
26	396.6	20.0	1080	3	US-08-629-335B-5
27	389	19.6	1338	2	US-08-044-812A-3

Sequence 3, Appli
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Sequence 11, Appli
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Sequence 3, Appli
Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-08-662-560-1

; Sequence 1, Application US/08662560

; Patent No. 5908609

; GENERAL INFORMATION:

; APPLICANT: Lee, Frank

; APPLICANT: Huszar, Dennis

; APPLICANT: Wei, Gu

; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS

; TITLE OF INVENTION: USEFUL IN THE REGULATION OF BODY WEIGHT

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036/2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/662,560

; FILING DATE: 10-JUN-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 7853-060

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-790-9090

; TELEFAX: 212-869-8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1671 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: Coding Sequence

; LOCATION: 394...1389

; OTHER INFORMATION:

US-08-662-560-1


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RESULT 3
US-08-870-511-5
; Sequence 5, Application US/08870511
; Patent No. 6287763
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank
; APPLICANT: Huszar, Dennis
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE
; TREATMENT OF OBESITY
; FILE REFERENCE: 7853-083
; CURRENT APPLICATION NUMBER: US/08/870, 511
; CURRENT FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 5
; LENGTH: 1671
; TYPE: DNA
; ORGANISM: Homo sapiens

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Db 1468 CTGCAACAGCTTTCTCTCCGTGAGGTACTGTGTTGAG-ATATCCATTGTGTAATTTA 1526
Qy 1579 ACTTATGATGTTTGTGATGTAAGAAAAAATGCCAGGCTCTGTA-CATTGCTAAATGTC 1637
Db 1527 AGCCTATGATTTT-ATGAGAAAAAATGCCAGTCTCTGATATTATTTCCAATCTC 1581
Qy 1638 ATGCTAC-TTTTGGGCTGTGCTTTGTTAATCCAT-TTCGAGGCTGTAGACACTTTGAATT 1695
Db 1582 ATGCTACTTTTGGCCATAAAATATCAATCTATGTTATAGTTGTAGGCACTGTGGATT 1641
Qy 1696 TCTAGAAAAGAA 1708
Db 1642 TACAAAAAGAAA 1654

RESULT 6

US-08-671-525B-7

; Sequence 7, Application US/08671525B

; Patent No. 5703220

; GENERAL INFORMATION:

; APPLICANT: Yamada, Tadataka

; APPLICANT: Gantz, Ira

; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.

; STREET: P.O. Box 828

; CITY: Bloomfield Hills

; STATE: MI

; COUNTRY: US

; ZIP: 48303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; FILING DATE: June 27, 1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, DeAnn F.

; REGISTRATION NUMBER: 36683

; REFERENCE/DOCKET NUMBER: 2115-000853DVB

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (810)641-1600

; TELEFAX: (810)641-0270

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 996 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..996

US-08-671-525B-7

Query Match

Best Local Similarity 41.2%; Score 817.4; DB 1; Length 996;

Matches 881; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

Qy 455 CACCCTTCAGCACCGAATGACACTTCTCTCCACTTCTGGAACGGCAGCCTACGGACA 514

Db 9 CTCACCCACCGTGGGATGACACTTCTCTGCACCTCTGGAACGGCAGCAGTTACAGACT 68

Qy 515 GCAGGCAACGCCACTGAGTCCCTTGGCAAAGGCTACCCCGACGGGGATGCTACGAGCA 574

RESULT 7

US-08-672-109B-7

; Sequence 7, Application US/08672109B

; Patent No. 5710265

; GENERAL INFORMATION:

; APPLICANT: Yamada, Tadataka

; APPLICANT: Gantz, Ira

; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors

; NUMBER OF SEQUENCES: 23

	Query Match	41.2%	Score 817.4;	DB 2;	Length 996;	
	Best Local Similarity	89.3%;	Pred.	No. 9.3e-190;		
	Matches 881;	Conservative	0;	Mismatches 106;	Indels	0; gaps 0;
Qy	455	CACCCCTTCAGCAGGGAATGCACACTTCTCTCCACTTTCTGGAAACCGCAGCACCTTACGACA	514			
Dd	9	CTCACCCCACGTGGGATGCACACTTCTCTGCACTTCTTGGAACCGCAGCATGTTACAGACT	68			
Qy	515	GCAAGGCCAAGCCACTGATGTCCTTGGCAAAGGCTACCCGACGGGGGATGCTTACAGACA	574			
Dd	69	GCACAGCAATTGCAGTGCAGTCCCTTTGGAAAAGGCTACTCTGATGGAGGGTGCTTACGACA	128			


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QY 575 ACTCTTCGTCCTCCCGAGGTGTTCTGACTCTGGGGTCATAAGCTTCTGGAGAACAT 634
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Db 129 ACTTTTGTCTCTCCCTGAGGTGTTTGTGACTCTGGGTGCATCAGCTTCTGGAGATAT 188

QY 635 TCTGGTGATCGTGGCAATAGCCAAAGAAATCTGCACCTCACCACATGACTTTTTCAT 694
  | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
Db 189 CTTAGTGATTTGGCAATAGCCAAAGAAATCTGCATTCACCATGACTTTTTCAT 248

QY 695 CTGTAGCTGGCTGTGGCCGATATGCTGTGAGCGTTTCCAAAGGTGCAGACCATCGT 754
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Db 249 CTGACGCTGGCTGTGGCTGATATGCTGTGAGCGTTTCAATGGATCAGAACCATAT 308

QY 755 CATCACCTTGTGAACAGTAGGATACGAGCGGAGAGTTTACGGTGAATATTGATAA 814
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Db 309 CATCACCTTATAACAGTAGGATACGAGCGGATACGAGTTTACAGTGAATATTGATAA 368

QY 815 TGTCAATTGACGCGGTGATCTGTAGTCTCTTGCCTCCCTGATTTGACGCTGCTCTCAAT 874
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Db 369 TGTCAATTGACGCGGTGATCTGTAGTCTCTTGCCTCCCTGATTTGACGCTGCTCTCAAT 428

QY 875 TGCAGTGCAGAGGTACTTTACTATCTTTTATGCCCTCCAGTACCATAACATCATGACGT 934
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Db 429 TGCAGTGCAGAGGTACTTTACTATCTTTTATGCCCTCCAGTACCATAACATCATGACGT 488

QY 935 GAGGGGGTTGGATCATCATCAGTTGCTGCGGGCTTGCACGGTGTGACGGTCTCT 994
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Db 489 TAAGGGGTTGGATCATCATCAAGTTGTTATGCGGAGCTTGCACGGTGTGACGGTCTCT 548

QY 995 GTTCATCTTACTCGGACAGTACTGCTGTCAATCTGCTCCCTCACCACATGTTCTTAC 1054
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Db 549 GTTCATCTTACTCAGATAGTACTGCTGTCAATCTGCTCCCTCACCACATGTTCTTAC 608

QY 1055 CATGCTGGCCCTCATGCTCTCTTACCTGCACATGTTCCCTCATGGCCAGACTGCACAT 1114
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Db 609 CATGCTGGCTCTCATGGCTCTCTCTATGTCACATGTTCCCTCATGGCCAGCTGCACAT 668

QY 1115 CAAGAGATCGCGCTCTCCCGGACCGGCAACCATCCGCAAGGGGCCAACATGAAGG 1174
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Db 669 TAAGAGGATGCTGCTCTCCCGGACCTGGTCCCATCGGCAAGGTGCAATGAAGG 728

QY 1175 TGGCATTACTTGACCATCTCTGTTGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1234
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Db 729 AGCGATTACTTGACCATCTCTGTTGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 788

QY 1235 CCACCTTGATATCTACATCTCTGTGCCCCAGAAATCCATCTGTGTGCTTCTCATGCTCA 1294
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Db 789 CCACCTTAATATCTACATCTCTGTGCCCCAGAAATCCATCTGTGTGCTTCTCATGCTCA 848

QY 1295 CTTTAACCTGTACCTCATCTGATCATGTGTAACTCCATFATCGACCCCTCTCATTTATGC 1354
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QY 1355 ACTCCGGAGCCAGAGCTGAGAAAACCTTCAAAGAGATCATCTGCTGCTATCTCTGCTGG 1414
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Db 909 ACTCCGGAGTCAAGAACTGAGAAAACCTTCAAAGAGATCATCTGCTGCTATCTCTGCTGG 968

QY 1415 TGGCCTTTGTGACTTGTCTAGCAGATA 1441
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Db 969 AGGCTTTGTGACTTGTCTAGCAGATA 995
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RESULT 10
US-08-629-335B-7
; Sequence 7, Application US/08629335B
; Patent No. 6117975
; GENERAL INFORMATION:
; APPLICANT: Yamada, Tadataka
; APPLICANT: Gantz, Ira
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
```

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STREET: P.O. Box 828
CITY: Bloomfield Hills
STATE: MI
COUNTRY: US
ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/629,335B
FILING DATE: July 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, DeAnn F.
REGISTRATION NUMBER: 36683
REFERENCE/DOCKET NUMBER: 2115-000853DVA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810)641-1600
TELEFAX: (810)641-0270
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 996 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 1..996
US-08-629-335B-7
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Query Match 41.2%; Score 817.4; DB 3; Length 996;
Best Local Similarity 89.3%; Pred. No. 9.3e-190;
Matches 881; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

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QY 455 CACCCCTTCAGCAGCGAATGACACACTCTCTCCACACTTCTGGAAACCGCAGCACCTAGGACA 514
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Db 9 CTCACCCACCGCTGGGATGCACACTCTCTGACCTCTGGAAACCGCAGCATACAGACT 68

QY 515 GCACGGCAACGACCTAGTCCCTTGGCAAGGCTACCCGACGGGGATGCTACGAGCA 574
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QY 575 ACTCTTCGTCCTCCCGAGGTGTTCTGACTCTGGGGTCAATAAGCTTGTCTGGAGAACAT 634
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Db 129 ACTTTTGTCTCTCCCTGAGGTGTTTGTGACTCTGGGTGTCTACAGCTTGTGGAGATAT 188

QY 635 TCTGTGATCTGGCAATAGCCAAAGAAATCTGCACCTCACCACATGACTTTTTCAT 694
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Db 189 CTTAGTGATTTGGCAATAGCCAAAGAAATCTGCATTCACCATGACTTTTTCAT 248

QY 695 CTGTAGCTGGCTGTGGCCGATATGCTGTGAGCGCTTCCAAAGGTGCAGACCATCGT 754
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 249 CTGACGCTGGCTGTGGCTGATATGCTGTGAGCGCTTCAATGGATCAGAACCATAT 308

QY 755 CATCACCTTGTGAACAGTAGGATACGAGCGGAGAGTTTACGGTGAATATTGATAA 814
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Db 309 CATCACCTTATAACAGTAGGATACGAGCGGATACGAGTTTACAGTGAATATTGATAA 368

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Db 369 TGTCAATTGACGCGGTGATCTGTAGTCTCTTGCCTCCCTGATTTGACGCTGCTCTCAAT 428

QY 875 TGCAGTGCAGAGGTACTTTACTATCTTTTATGCCCTCCAGTACCATAACATCATGACGT 934
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 429 TGCAGTGCAGAGGTACTTTACTATCTTTTATGCCCTCCAGTACCATAACATCATGACGT 488
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Qy	935	GAGCGGGTTGGGATCATCATCTGCGCGGCTTGCACGTGTCACGGTGTGCACGGTGTGCACGGATCTTT	994
Db	489	TAAGCGGGTTGGGATCATCAAGTTGTATCTGGGCAGCTTGCACGGTGTGCACGGATTTT	548
Qy	995	GTTTCATCATTTACTCGGACAGTACTGCTGTGCATCATCTGCCTCATCACCATGTTCTTCAC	1054
Db	549	GTTTCATCATTTACTCGGACAGTACTGCTGTGCATCATCTGCCTCATCACCATGTTCTTCAC	608
Qy	1055	CATGCTGGCCCTCATGGCTTCTCTCTACGTCCACATGTTCTCATGCGCCAGACTGCACAT	1114
Db	609	CATGCTGGCTCTCATGGCTTCTCTCTATGTCCACATGTTCTGATGCGCAGGCTTCACAT	668
Qy	1115	CAGAGAAATCGCGTCTCCCGGCGCACCGCACCATCCGCGAAGGGGCCAACATGGAAGG	1174
Db	669	TAAGAGAAATGCTGTCTCCCGGCGACTGGTGCCATCCGCGAAGGTGCCAATATGAAGG	728
Qy	1175	TGCATTAACCTTGACCATACTCATTTGGGGTCTTCGTGCTGCTGGGCTCCATTCCTTCT	1234
Db	729	AGCAATTAACCTTGACCATACTGATGGGCTTTGTGCTGCGGGCCCATCTCTTCT	788
Qy	1235	CCACTTGATATTTACATCTCTTGTCGCCAGAAATCCATACTGTGTGTGCTTCATGTCTCA	1294
Db	789	CCACTTAATATTTACATCTCTTGTCGCCAGAAATCCATAATTTGTGTGTGCTTCATGTCTCA	848
Qy	1295	CTTTAACTTGTACCTCATTTCTGATCATGTGTAACTCCATCATCGACCTCTCATTTATGC	1354
Db	849	CTTTAACTTGTATCTCTCATCTGATCATGTGTAAATTCATCATCGATCCTCTGATTTATGC	908
Qy	1355	ACTCCGGAGCAAGAGCTGAGGAAACCTTCAAAGAGATCATCTGTTGCTATCCTCTGGG	1414
Db	909	ACTCCGGAGTCAAGAACTGAGGAAACCTTCAAAGAGATCATCTGTTGCTATCCTCTGGG	968
Qy	1415	TGGCCTTTGTGACTTGTCTAGCAGATA	1441
Db	969	AGGCCTTTGTGACTTGTCTAGCAGATA	995
RESULT 11			
US-08-870-511-7			
; Sequence 7, Application us/08870511			
; Patent No. 6287763			
; GENERAL INFORMATION:			
; APPLICANT: Lee, Frank			
; APPLICANT: Huszar, Dennis			
; APPLICANT: Gu, Wei			
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE			
; TITLE OF INVENTION: REGULATION OF BODY WEIGHT			
; FILE REFERENCE: 7853-083			
; CURRENT APPLICATION NUMBER: US/08/870,511			
; CURRENT FILING DATE: 1997-06-06			
; NUMBER OF SEQ ID NOS: 45			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 7			
; LENGTH: 999			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (1)..(996)			
US-08-870-511-7			

Qy	575	ACTCTTCGCTCCCCGGAGGTGTTCTGTGACTCTGGGGGTCAATAAGCTTGCTGGAGAACAT	634
Db	129	ACTTTTGTCTCTCCCTGAGGTGTTGTGTGACTCTGGGTGCATCAGCTTGTTGGAGAATAT	188
Qy	635	TCGTGGTGATCGTGGCAATAGCCAAGAACAAAGAAATCTGCACCTCACCCATGACTTTTTCAT	694
Db	189	CTTAGTGATTTGTGGCAATAGCCAAGAACAAAGAAATCTGCATTTACCCATGACTTTTTCAT	248
Qy	695	CTGTAGCTCGCTGTGGCCGATATGCTGTGTGAGCGTTTCCAAACGGTGCAGACCACTCGT	754
Db	249	CTGCAGCTTGGCTGTGGCTGATATGCTGTGTGAGCGTTTCAATGTGAATCAAAACCAATAT	308
Qy	755	CATCACCCCTGTTGAACAGTACGGATACGGACGCGCAGAGTTTCCACGGTGAATATTGATAA	814
Db	309	CATCACCCCTATTAAACAGTACAGATACGGATGCACAGAGTTTCCACAGTGAATATTGATAA	368
Qy	815	TGTCATTGACTCGGTGATCTGTAGTACCTTGTCTGGCTCGATTTTGACGCTGCTCTCAAT	874
Db	369	TGTCATTGACTCGGTGATCTGTAGTACCTTGTCTGGCTCGATTTTGACGCTGCTCTCAAT	428
Qy	875	TGCAGTGCAGGTACTTTTACTATCTTTTATGCGCTCCAGTACCATAAATCATGATACGGT	934
Db	429	TGCAGTGCAGGTACTTTTACTATCTTTTATGCGCTCCAGTACCATAAATCATGATACAGT	488
Qy	935	GAGCGGGTTGGGATCATCATCAGTTCATCTGGGGGGTGTGACGGTGTTCAGGCATCTT	994
Db	489	TAAGCGGGTTGGATCAGCATAGTTGTATCTGGGCAGCTTGCACGGTTTCAGGCATTTT	548
Qy	995	GTTTCATCATTTTACTCGGACAGTACTGCTGTATCATCTGCGCTCATCACCATGTTCTTCAC	1054
Db	549	GTTTCATCATTTTACTCGATAGTGTGTGTATCATCTGCGCTCATCACCATGTTCTTCAC	608
Qy	1055	CATGCTGGCCCTCATGGCTTCTCTACGTCCACATGTTCCCTCATGGCCAGAGCTGCACAT	1114
Db	609	CATGCTGGCTCTCATGGCTTCTCTATGTATGTCACATGTTCCCTGATGCCAGGCTTCACAT	668
Qy	1115	CAAGAGAAATCGCGTCTCTCCGGGCACCGCACCATCCGCAAGGGGCCAAACATGAAGG	1174
Db	669	TAAGAGGATTTGCTGTCTCCCGGCACTGGTGCCATCCGCAAGGTGCCAATATGAAGGG	728
Qy	1175	TGCCATPACCTTGACCATACTCATTTGGGGTCTTGTGCTGCTGGGCTCCATTTCTCCT	1234
Db	729	AGCGATTACCTTGACCATCTGATTTGGGGTCTTTGTTGTCTGCTGGGCCCATCTTCTCT	788
Qy	1235	CCACTTGATATTCTACATCTTTGTCGCCAGAAATCCATACTGTGTGTGCTCATGTCTCA	1294
Db	789	CCACTTAATATTCTACATCTTTGTCCTCCAGAAATCCATATTGTGTGTGCTTCTGCTCA	848
Qy	1295	CTTTAACTTCTACTCATTTCTGATCATGTGTAACTCCATCATCGACCCCTCTCATTTATGC	1354
Db	849	CTTTAACTTGTATCTCATACTGATCATGTGTAAATTCATATCATCGATCCCTCTGATTTATGC	908
Qy	1355	ACTCCGGAGCAAGAGCTAGGAAAAACCTTCAAAGAGATCATCTGTTGCTATCCTCTGG	1414
Db	909	ACTCCGGAGTCAAGAACTGAGGAAAAACCTTCAAAGAGATCATCTGTTGCTATCCCCCTGG	968
Qy	1415	TGGCCTTTGTGACTTGTCTAGACAGTACTA	1444
Db	969	AGGCCTTTGTGACTTGTCTAGCAGATATTA	998

RESULT 12
US-08-870-511-9
: Sequence 9, Application US/08870511
: Patent NO. 6287763
: GENERAL INFORMATION:
: APPLICANT: Lee, Frank
: APPLICANT: Huszar, Dennis
: APPLICANT: Gu, Wei
: TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE
: TREATMENT OF OBESITY
: TITLE OF INVENTION: REGULATION OF BODY WEIGHT
: FILE REFERENCE: 7853-083
: CURRENT APPLICATION NUMBER: US/08/870, 511

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; CURRENT FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 9
; LENGTH: 999
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(996)
US-08-870-511-9

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Query Match	41.1%	Score	815.6	DB 4	Length	999			
Best Local Similarity	89.0%	Pred.	No. 2.5e-189						
Matches	881	Conservative	0	Mismatches	109	Indels	0	Gaps	0

QY	455	CACCCCTTCAGCAGCGGATGCACACTTCTCTCCACTTCTGGAACCGGACGACCTTACGGACA	514
DB	9	CTCACCCACCGTGGGATGCACACTTCTCTGCACCTCTGGAACCGGACGAGTTACACACT	68
QY	515	GCACGGCAGCGCACATGAGTCCCTTGGAAGAAGCTACCCGACGGGGGATGCTACGAGCA	574
DB	69	GCACAGCATGCCAGTAGTCCCTTGGAAGAAGCTACTCTGATGGAGGGTGTCTACGAGCA	128
QY	575	ACTCTTCGTCTCCCCGAGGTGTTCGTGACTCTGGGGGTCTAATAGCTTGTCTGGAGAACAT	634
DB	129	ACTTTTTGTCTCTCCGTAGGTGTTGTGACTCTGGGTGTCTATCAGCTTGTGGAGATAT	188
QY	635	TCTGGTGATCTGGCAATAGCCAAAGAACAAAGATCTGCACTCACCCANGTACTTTTTTCAT	694
DB	189	CTTAGTGATTTGGCAATAGCCAAAGAACAAAGATCTGCATTCCACCATGCTACTTTTTTCAT	248
QY	695	CTCTAGCCTGGCTGGCCGATATGCTGGTGGGCTTTCACAGGGTTCAGAGACCATCGT	754
DB	249	CTGCACCTTGGCTGGCTGGATGCTGGTGGGCTTTCAAATGGATTCAGAAACCATAT	308
QY	755	CATCACCCCTTTGAACAGTACGGATACGGACGGCCAGAGTTTCACGGTGAATATTGATAA	814
DB	309	CATCACCCCTATTAAACAGTACAGATATGGATGACACAGAGTTTCACAGTGAATATTGATAA	368
QY	815	TGTCATTGACTCGGTGATCTGTAGTCTTGTCTGGCTTCGATTTGCAAGCCTGCTCTCAAT	874
DB	369	TGTCATTGACTCGGTGATCTGTAGTCTTGTCTGGCTTCGATTTGCAAGCCTGCTCTCAAT	428
QY	875	TGCAGTGGACAGTACTTTACTATCTTTATGCGCTCCAGTACCATAACATCATGACGT	934
DB	429	TGCAGTGGACAGTACTTTACTATCTTTATGCTCTCCAGTACCATAACATTTAGACGT	488
QY	935	GAGCGGGTTGGGATCATCATGATTGCATCTGGGGGGCTTGCACGGTGTGCAGGCATCTT	994
DB	489	TAAGCGGGTTGGGATCAGCATAGTTGTATCTGGGCAGCTTGCACGGTTTCAGGCATTTT	548
QY	995	GTTTCATATTACTCGGACAGTACTGCTGTCAATCTGCCTCATCACCAGTGTCTTCAC	1054
DB	549	GTTTCATATTACTCAGATAGTGTCTGTCAATCTGCCTCATCACCAGTGTCTTCAC	608
QY	1055	CATGCTGGCCCTCATGGCTTCTCTACGTCCACATGTTCTCATGCGCCAGACTGCACAT	1114
DB	609	CATGCTGGCTCATGGCTTCTCTCATGTCCACATGTTCTCATGCGCCAGGCTTCACAT	668
QY	1115	CAAGAGAAATCGCGTCTCTCCGGGACCGGCACCATCCGCAAGGGGCCAACATGAAGG	1174
DB	669	TAAGAGGATTGCTGTCTCTCCCGGCACTGGTGGCATCCGCAAGGTGCCAATATGAAGG	728
QY	1175	TGCCAATTACCTTGACCATACTCATTTGGGGTCTTCGTCGTCTGCTGGGCTCCATTCCTCCCT	1234
DB	729	AGCGAATTACCTTGACCATCTGATTGGCGTCTTTGTGTCTGCTGGGCCCATTCCTCCT	788
QY	1235	CCACTTGATATTCTACATCTCTTGCCCCAGAAATCCATACTGTGTGTGCTTCATGCTCA	1294
DB	789	CCACTTGATATTCTACATCTCTTGCTCCAGAAATCCATATTGTGTGTGCTTCATGCTCA	848
QY	1295	CTTTAACTTGTAACCTCATCTCATGTGAATCTCAATCATCTGACCCCTCTCATTTATGC	1354

Db	849	CTTTAACTTGATCTCATCATGATCATGTGTAATTCATCATCATCTCTGATTATGC	908
Qy	1355	ACTCCGGAGCAAGAGCGTGGAGGAAAACCTTCAAAGAGATCATCTGTTGCTATCTCTGGG	1414
Db	909	ACTCCGGAGTCAAGACTGAGGAAAACCTTCAAAGAGATCATCTGTTGCTATCTCCCTGGG	968
Qy	1415	TGGCCTTTGTGACTGTGCTAGCAGATACTA	1444
Db	969	AGGCCTTTGTGACTTGTCTAGCAGATATTA	998

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RESULT 13
US-08-870-511-11
; Sequence 11, Application US/08870511
; Patent No. 6287763
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank
; APPLICANT: Huszar, Dennis
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE
; TREATMENT OF OBESITY
; FILE REFERENCE: 7853-083
; CURRENT APPLICATION NUMBER: US/08/870,511
; CURRENT FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 999
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(996)
; US-08-870-511-11

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Query Match	41.1%	Score 815.6	DB 4	Length 999
Best Local Similarity	89.0%	Pred. No. 2.5e-189		
Matches 881	Conservative 0	Mismatches 109	Indels 0	Gaps 0
QY	455	CACCCCTTCACACGGGAATGCACACTTCTCTCCACTTCTGGAAACCGCAGCACTACGAGCA	514	
Db	9	CTCCACCACCGTGGGAATGCACACTTCTGCACTCTGGAAACCGCAGCACTTACAGACT	68	
QY	515	GCACGGCAGCCCACTCAGTCCCTTGGCAAGGCTACCCGACGCGGGGATGCTACGAGCA	574	
Db	69	GCACGAATGCCAGTGAGTCCCTTGGAAAGGCTACTCTGATCGAGGGTCTACGAGCA	128	
QY	575	ACTCTTGGTCTCCCCGGAGGTGTCGTGACTCTGGGGGTCAATAGCTTGCTGGAGAACAT	634	
Db	129	ACTTTTGTCTCTCTGAGGTGTTGTGACTCTGGGTGTCATCAGCTTGTGGAGAAAT	188	
QY	635	TCGTGGTGATCGTGGCAATAGCCAAAGAACAAAGATCTGCATCACCATGCTATTTTTCAT	694	
Db	189	CTTAGTGATTTGGCAATAGCCAAAGAACAAAGATCTGCATTCACCCATGCTATTTTTCAT	248	
QY	695	CTCTAGCCTGGCTGTGGCCCATATGCTGGTGAGGTTTCCAAAGGGTTCAGAGCAACATCGT	754	
Db	249	CTCAGCTTGGCTGTGGCTGATATGCTGGTGAGCGTTTTCAATTTGGAATCGAAACCAATAT	308	
QY	755	CATCACCCCTTTTGAACAGTACGGATACGGACGCGCAGAGTTTCCAGGTGAATATTGTATAA	814	
Db	309	CATCACCCCTATTAAACAGTACAGATATGGATGCACAGAGTTTTCACAGTGAATATTGTATAA	368	
QY	815	TGTCATTTGACTCGGTGATCTGTTAGTCCTTGGCTTCGGCTCGATTTGCAAGCCTGCTCTCAAT	874	
Db	369	TGTCATTTGACTCGGTGATCTGTTAGTCCTTGGCTTCGGCTCGATTTGCAAGCCTGCTCTCAAT	428	
QY	875	TGCAGTGGACAGTACTTTTACTATCTTTTATGCTCCCTCCAGTACCATAACATCATGACGGT	934	
Db	429	TGCAGTGGACAGTACTTTTACTATCTTTTATGCTCCCTCCAGTACCATAACATTTTATGACGT	488	
QY	935	GAGGCGGGTGGGATCATCATCAGTTGCACTCTGGGCGGCTTGCACGGTGTTCAGGCATCTTT	994	

Db 489 TAAGCGGTTGGGATCAGCATAAGTTGATCTGGGAGCTTGCACGGTTTCAGGCAATTT 548
Qy 995 GTTCATCATTTACTCGGACAGTACTGCTGTCATCATCTGCTCATCATCACCATTGTTCTTCAC 1054
Db 549 GTTCATCATTTACTCAGATAGTAGTGTGTCATCATCTGCTCATCATCACCATTGTTCTTCAC 608
Qy 1055 CATGCTGGCCCTCATGCTTCTCTCTACGTCACATGTTCTCATGCGCCAGACTGTCACAT 1114
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Qy 1115 CAGAGAAATCCCGTCTCCGGGACACGGGACACATCCGCCAAGGGCCCAACATGAAGG 1174
Db 669 TAAGAGGATTGCTGCTCCCGGCACTGGTGCCATCCGCCAAGGTGCCAATATGAAGG 728
Qy 1175 TGCCATTACCTTGACCAATACCTCATTTGGGTCCTGCTGCTGCTGCTGCTGCTGCTGCT 1234
Db 729 AGGATTAACCTTGACCAATACCTCATTTGGGTCCTGCTGCTGCTGCTGCTGCTGCTGCT 788
Qy 1235 CCACCTGATATTTACATCTCTTGTCCCGAATCCATACTGTGTGCTTCAATGCTCA 1294
Db 789 CCACCTAATATTTACATCTCTTGTCCCGAATCCATACTGTGTGCTTCAATGCTCA 848
Qy 1295 CTTTAACCTTGACCAATACCTCATTTGGGTCCTGCTGCTGCTGCTGCTGCTGCTGCT 1354
Db 849 CTTTAACCTTGATCTATCTACTGATCATGTGTAATTCATCATCATCATCATCATCAT 908
Qy 1355 ACTCCGGAGCAAGAGCTGAGGAAACCTTCAAGAGATCATCTGTTGCTATCCTCTCGG 1414
Db 909 ACTCCGGAGCAAGAGCTGAGGAAACCTTCAAGAGATCATCTGTTGCTATCCTCTCGG 968
Qy 1415 TGGCCTTTGACTTGTCTAGCAGATACTA 1444
Db 969 AGGCTTTGACTTGTCTAGCAGATATTA 998

RESULT 14

US-08-671-525B-9
; Sequence 9, Application US/08671525B
; Patent No. 5703220
; GENERAL INFORMATION:
; APPLICANT: Yamada, Tadataka
; APPLICANT: Gantz, Ira
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: US
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/671,525B
; FILING DATE: June 27, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, DeAnn F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-000853DVB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 975 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1...975
US-08-671-525B-9

Query Match 21.5%; Score 426.2; DB 1; Length 975;
Best Local Similarity 68.6%; Pred. No. 1.6e-94;
Matches 603; Conservative 0; Mismatches 273; Indels 3; Gaps 1;

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RESULT 15

US-08-672-109B-9

; Sequence 9, Application US/08672109B

; Patent No. 5710265

; GENERAL INFORMATION:

; APPLICANT: Yamada, Tadataka

; APPLICANT: Gantz, Ira

; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS: 23

; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.

; STREET: P.O. Box 828

; CITY: Bloomfield Hills

; STATE: MI

; COUNTRY: US

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; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/672,109B

; FILING DATE: June 27, 1996

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, Deann F.

; REGISTRATION NUMBER: 36683

; REFERENCE/DOCKET NUMBER: 2115-000853DVC

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (810)641-1600

; TELEFAX: (810)641-0270

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 975 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; HYPOPHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Mouse

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..975

; US-08-672-109B-9

Query Match 21.5%; Score 426.2; DB 1; Length 975;

Best Local Similarity 68.6%; Pred. No. 1.6e-94;

Matches 603; Conservative 0; Mismatches 273; Indels 3; Gaps 1;

QY 566 CTACGAGCAACTCTCGTCTCCCGGAGGTGTCGACTCTGGGGGTCAATAAGTTGCT 625

Db 96 CTGTGAAGAAATGGGCAATTCGCGTGGAGGTTCCTCGACCCCTGGGTCTCGTCAGCCTCTT 155

QY 626 GGAGAACATTCGTGGTGGTGGCAATAGCCCAAGAACAGAGATCTGCACCTACCCATGTA 585

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QY 1043 CATGTTCTTCACCATGCTGCGCCTCATGCTCTCTCTCTAGTCCACATGTTCTCTCATGGC 1102

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Db 936 TCACGGATTCCGGCGACCTTGTAGGCTCCTTGGCGGGTA 974

Search completed: June 14, 2003, 10:34:02

Job time : 89 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 14, 2003, 11:43:44 ; Search time 321 seconds
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Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1165.6	58.7	1708	24	ABK15577 DNA encoding felin
3	958.2	48.3	1671	24	AAD25896 Human melanocortin
4	957.8	48.3	1671	24	AAD25930 Human melanocortin
5	939	47.3	1671	19	AAV19142 Human melanocortin
6	939	47.3	1671	20	AAV63707 Human melanocortin
7	818.8	41.2	999	22	AAAF85465 Nucleotide sequenc
8	817.6	41.2	1030	21	AAA26972 Rhesus monkey mela
9	817.4	41.2	996	18	AAV68790 Melanocortin-4 rec

10	817.4	41.2	996	19	AAV62352 Melanocortin-4 rec
11	817.4	41.2	996	19	AAV06400 Human melanocortin
12	817.4	41.2	996	20	AAV01964 Human MC4 DNA. Ho
13	817.4	41.2	996	21	AAA75829 DNA encoding a hum
14	817.2	41.2	999	21	AAA46089 Human G protein co
15	817.2	41.2	999	24	AAD25897 Human melanocortin
16	814	41.0	999	21	AAA46119 Human G protein co
17	806	40.6	999	19	AAV03252 Homo sapiens DNA e
18	802.8	40.4	999	19	AAV03253 Homo sapiens DNA e
19	798	40.2	999	19	AAV03251 Homo sapiens DNA e
20	703.6	35.4	840	22	AAV03251 Homo sapiens DNA e
21	637.2	32.1	746	21	AAV03251 Homo sapiens DNA e
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24	437.2	22.0	1599	16	AAO97701 Rat melanocortin r
25	432.4	21.8	1262	16	AAO97702 Human melanocortin
26	428.2	21.6	1080	21	AAV27402 Rhesus monkey mela
27	428.2	21.6	1081	21	AAV15583 Rhesus monkey mela
28	426.2	21.5	975	18	AAV68791 Melanocortin-5 rec
29	426.2	21.5	975	19	AAV62353 Melanocortin-5 rec
30	426.2	21.5	975	19	AAV03916 Mouse melanocortin
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34	426	21.5	978	19	AAV19143 Mouse melanocortin
35	426	21.5	978	20	AAV63708 Mouse melanocortin
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37	408.2	20.6	1909	21	AAV27110 Rhesus monkey mela
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ALIGNMENTS

RESULT 1

ABK15578

ID ABK15578 standard; cdna; 1985 BP.

AC ABK15578;

DT 08-MAY-2002 (first entry)

DE DNA encoding canine melanocortin 4 receptor (MC4R).

KW Melanocortin 4 receptor; MC4R; G-protein coupled receptor; dog;
KW appetite; metabolic disorder; cachexia; anorexia;
KW weaning-induced inappetence; growth; diabetes; cancer; renal failure;
KW cardiac disease; endotoxaemia; fever; hepatic lipodosis; infection;
KW inflammation; post partum sow; dairy cow; livestock; poultry;
KW shipping stress; crowding stress; obesity; vaccine; gene; ss.

OS Canidae.

FH Key Location/Qualifiers

FT CDS 447..1445

FT **tag= a

FT /product= "MC4R"

FT /note= "Melanocortin 4 receptor"

FT EPI167386-A1.

PD 02-JAN-2002.

XX 26-JUN-2001; 2001EP-0305509.

XX 26-JUN-2000; 2000US-213909p.

PR


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RESULT 3

AAD25896

ID AAD25896 standard; DNA; 1671 BP.

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XX AAD25896;
XX 26-MAR-2002 (first entry)
XX Human melanocortin 4-receptor (MC4R) gene #1.
DE Human; single nucleotide polymorphism; SNP; melanocortin 4-receptor;
KW MC4R; haplotype; obesity; screening; allele-specific oligonucleotide;
KW ASO; gene therapy; anorectic; chromosome 18q22; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
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FT /number= 1
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XX WO200179222-A2.
XX 25-OCT-2001.
XX 12-APR-2001; 2001WO-US11943.
XX 12-APR-2000; 2000US-196677P.
XX (GENA-) GENAISSANCE PHARM INC.
XX Bentivegnà SC, Choi JY, Kazemi A, Lee HH, Nandabalan K, Parks KE;
XX Sausker EA;
XX WPI: 2002-082744/11.
XX P-PSDB; AAE15746.
XX Novel polymorphic variants of melanocortin 4-receptor gene useful in
XX studying expression and function of the protein, useful for screening
XX candidate drugs to treat diseases related to the protein activity e.g.
XX obesity
XX Claim 19; Fig 1; 53pp; English.
XX The invention relates to single nucleotide polymorphisms (SNP) in human
XX melanocortin 4-receptor (MC4R) gene. MC4R gene haplotypes are useful
XX for improving the efficiency and reliability of several steps in the
XX discovery and development of drugs for treating diseases associated
XX with MC4R activity, e.g. obesity. MC4R gene is useful in studying the
```


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QY 1101 GCCAGACTGCACATCAAGAGAAATCGCGTCTCCCGGACCGGACCGCACCCGCAAGGG 1160
Db 1048 GCCAGGCTTCACATTAAGAGGATGTGCTCTCCCGGACCTGGTGCATCCGCAAGGT 1107
QY 1161 GCCAACATGAAGGTTGCCATTTACCTTGACCATACTCAFTTGGGGTCTTCGTCTGCTGCTGG 1220
Db 1108 GCCAATATGAAGGAGCGATTAACCTTGACCATCTGATTTGGCGCTTTGTTGTCTGCTGG 1167
QY 1221 GCTCATCTTCTCCCACTTGATATCTACATCTCTGTTGCCAGAAATCCATAGTGTGTG 1280
Db 1168 GCCCATCTTCTCCCACTTAATATCTACATCTCTTGTCTCCAGAAATCCATATGTTGTG 1227
QY 1281 TGCTTCATGCTCACTTTAACTTGTACCTTATCTGATCATGCTGTAACTCCCATCATCCAC 1340
Db 1228 TGCCTCATGCTCACTTTAACTTGTATCTCATCTGATCATGTTGTTAAATCAATCATCAT 1287
QY 1341 CCTCTCAFTTTATGCACTCCGAGGCAAGAGCTGAGGAAACCTTCAAGAGATCATCTGT 1400
Db 1288 CCTCTGATTTATGCACTCCGAGTCAAGAACTGAGGAAACCTTCAAGAGATCATCTCT 1347
QY 1401 TGCTATCTCTGGTGGCTTTGAGCTTGTGCTAGCAGATACTAGCTGGGACAGAGAA 1460
Db 1348 TCCTATCCCTTGGGAGGCTTTGTGACTTGTCTAGCAGATATTAATTAATGGGACAGCAC 1407
QY 1461 GTACTAAA--AACATGCCACAGACACTTCTTCATCCCTCACACATCAATCAATGTTGCTT 1518
Db 1408 GCAATATAGGAACATCCCAAGAGACTTTTTCAGTCTTACCTCTTACCTCTACCTGAATTTCTACTT 1467
QY 1519 GGACAACAGCTGCTTCTTCACTATAAGGCGAGGTGAGATAATCTGTTGCACAAATCA 1578
Db 1468 CTGCAACAGCTTTCTCTCCGTGTAGGCTACTGTTGAG-ATATCCATGTTGTTAAATTA 1526
QY 1579 ACTTTATGATGTTTGTGTAAGAAAAAATGCCAGGCTCTGTA-CATTGCTAAATGTC 1637
Db 1527 AGCCTATGATTTTTT-----AATGAGAAAAAATGCCAGTCTCTGTATTTATTTCCAAATCTC 1581

QY 1638 ATGCTAC-TTTTGGCTGTGCATTTAATCCAT-TTCGAGCTGTAGACACTTTGAATT 1695
Db 1582 ATGCTACTTTTGGCCATAAATATGAATCTATGCTTATAGTTGTAGCCACTCTGGATT 1641
QY 1696 TCTAGAAAGAAA 1708
Db 1642 TACAAAAGAAAA 1654
RESULT 7
AAF85465
ID AAF85465 standard; DNA; 999 BP.
XX AAF85465;
XX
DT 23-JUL-2001 (first entry)
XX Nucleotide sequence of a human melanocortin-4 receptor (MC-R4).
DE Human; melanocortin-4 receptor; MC-R4; transgenic animal; body weight;
KW food intake; obesity; diabetes; anorexia; cachexia; cancer;
KW sexual dysfunction; pain; impaired memory; neuronal regeneration;
KW neuropathy; growth disorder; growth hormone;
KW insulin-like growth factor-1; ss.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..999
FT /*tag= a
FT /*product= "melanocortin-4 receptor (MC-R4)"
XX
PN WO200133956-A1.
XX
PD 17-MAY-2001.
XX
PF 13-NOV-2000; 2000WO-US31061.
XX
PR 12-NOV-1999; 99US-0165074.
XX
PA (MERI) MERCK & CO INC.
XX
PI Van Der Ploeg LHT, Chen AS, Chen HV, Forrest MJ, MacIntyre DE;
PI Metzger JM, Palyha OC, Feighner SD, Hreniuk D;
XX
DR WPI; 2001-343541/36.
DR P-PSDB; AAB68490.
XX
PT New transgenic animal with non-functional gene for melanocortin-4
PT receptor, useful for identifying specific modulators, potentially used
PT for treating obesity or diabetes.
XX
PS Disclosure; Fig 1; 58pp; English.
XX
CC The present sequence encodes a human melanocortin-4 receptor (MC-R4).
CC The specification describes transgenic non-human animals whose somatic
CC and germ cells contain at least one non-functional gene for MC-4R
CC protein. The transgenic animals, or cells derived from them, are used
CC to screen for compounds that modulate MC-4R. These modulators are
CC potentially useful for regulating body weight and food intake and
CC treatment of associated diseases, obesity; diabetes; anorexia; cachexia;
CC cancer; sexual dysfunction; pain; impaired memory or neuronal
CC regeneration; neuropathy; growth disorders linked to growth hormone
CC and insulin-like growth factor-1. They can also be used to study MC-4R
CC expression and activity.
XX
SQ Sequence 999 BP; 229 A; 243 C; 213 G; 314 T; 0 other;

Query Match 41.2%; Score 818.8; DB 22; Length 999;
Best Local Similarity 89.2%; Pred. NO. 4.5e-184;
Matches 883; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

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QY 455 CACCCTTACGACGGAATGACACTTCTCTCCACTTCTGGAAACCGCAGACCTTACGACA 514
Db 9 CTCACCCACCGGTGGGATGACACTTCTCTGCACTCTGGAACCGCAGCATTTACAGACT 68
QY 515 GCACGGACGCGCCACTGAGTCCCTTGGCAAAAGGCTACCCGAGCGGGGATGCTACGAGA 574
Db 69 GCACAGCAATGCCAGTGAAGTCCCTTGGAAAGGCTACTCTGATGGAGGGTGTCTACGAGA 128
QY 575 ACTCTTCTGCTCCCGGAGGTGTCTGAGCTCTGGGGGTCAATAGCTTGTGGAGAACAT 634
Db 129 ACTTTTGTCTCTCCCTGAGGTGTCTGAGCTCTGGGTGTCTACAGCTTGTGGAGAAAT 188
QY 635 TCTGGTGAATGGGCAATAGCCAAAGAAATCTGCACCTACCCCATGTACTTTTTCAT 694
Db 189 CTTAGTGAATTTGGCAATAGCCAAAGAAATCTGCATTCACCCATGTACTTTTTCAT 248
QY 695 CTGTAGCCTGGCTGTGGCGGATATGCTGTGAGCGTTTCCAAAGGTCAGAGACCATCT 754
Db 249 CTGCAGCTTGGCTGTGGCTGTATGCTGTGAGCGTTTCAAATGGATCAGAAACCATTA 308
QY 755 CATCACCTTGTGAACAGTACGATACGGACGCGCAGAGTTTCAAGGTGAATATTGATAA 814
Db 309 CATCACCTTATAAACAGTACAGATACGATACGATGACAGAGTTTCAAGTGAATATTGATAA 368
QY 815 TGTCAATGACTCGGTGATCTGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 874
Db 369 TGTCAATGACTCGGTGATCTGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 428
QY 875 TGCAGTGGACAGTACTTTTACTATCTTTTATGCTTCCCTCCAGTACCATTAACATGACG 934
Db 429 TGCAGTGGACAGTACTTTTACTATCTTTTATGCTTCCCTCCAGTACCATTAACATGACAG 488
QY 935 GAGCGGGTGGGATCATCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 994
Db 489 TAAGCGGTGGATCATCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 548
QY 995 GTTCATATTTACTGGACAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1054
Db 549 GTTCATATTTACTGAGATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608
QY 1055 CATGTGGCCCTCATGCTCTCTCTACGTCCACATGTTCCCTCATGGCCAGACTGCACAT 1114
Db 609 CATGTGGCTCTCATGCTCTCTCTATGCTCCACATGTTCCCTCATGGCCAGCTTCACAT 668
QY 1115 CAAGAAATFCGCGCTCTCCCGGACCGGACACCATCCGCCAAGGGGCCAATGAAGGG 1174
Db 669 TAAGAGAGTTGCTCTCTCCCGGACCTGGTGCCATCGCCAAAGTGCCAAATATGAAGG 728
QY 1175 TGGCATTACCTTGACCATCAATTTGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1234
Db 729 AGCGATTACCTTGACCATCAATTTGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 788
QY 1235 CCACCTTGATATTTACTATCTCTGTTGCCAGAAATCCATCTGTGTGCTTCCATCTCA 1294
Db 789 CCACCTTGATATTTACTATCTCTGTTGCCAGAAATCCATCTGTGTGCTTCCATCTCA 848
QY 1295 CTTTAACCTTGATATTTACTATCTCTGTTGCCAGAAATCCATCTGTGTGCTTCCATCTCA 1354
Db 849 CTTTAACCTTGATATTTACTATCTCTGTTGCCAGAAATCCATCTGTGTGCTTCCATCTCA 908
QY 1355 ACTCCGGAGCCAGAGCTGAGGAAACCTTCAAGAGATCATCTGCTGCTGCTGCTGCTGCTGCT 1414
Db 909 ACTCCGGAGCTAAGAACTGAGGAAACCTTCAAGAGATCATCTGCTGCTGCTGCTGCTGCTGCT 968
QY 1415 TGGCCTTTGTGACTTGTCTAGCAGATACTA 1444
Db 969 AGGCCCTTTGTGACTTGTCTAGCAGATACTA 998
```

RESULT 8
AAA26972
ID AAA26972 standard; cDNA; 1030 BP.
XX

```
AC AAA26972;
XX 04-AUG-2000 (first entry)
XX Rhesus monkey melanocortin-4 receptor gene.
XX Rhesus monkey; rhodopsin; G-protein coupled receptor; anorectic;
KW melanocyte stimulating hormone; melanocortin receptor; obesity; ss.
XX Macaca mulatta.
XX Key Location/Qualifiers
FH 17..1015
FT CDS
FT /*tag= a
FT /product= "melanocortin-4 receptor protein"
XX WO200027863-A1.
XX 18-MAY-2000.
XX 05-NOV-1999; 99WO-US25767.
XX 09-NOV-1998; 98US-0107721.
XX (MERI ) MERCK & CO INC.
XX MacNeil DJ, Weinberg DH, Van Der Ploeg LHT;
XX WPI: 2000-376480/32.
XX P-PSDB; AAY94301.
XX Novel DNA encoding rhesus monkey melanocortin 4 receptor protein,
XX recombinant vectors and host cells, useful in methods for identifying
XX selective agonists and antagonists
XX Claim 1: Page 35; 53pp; English.
XX The present sequence encodes the rhesus monkey melanocortin-4
XX receptor protein (MC-4R). Melanocortin receptors belong to the
XX rhodopsin sub-family of G-protein coupled receptors. They bind and are
XX activated by peptides such as alpha-, beta-, or gamma-melanocyte
XX stimulating hormones derived from the pro-opiomelanocortin gene and they
XX are believed to mediate a wide range of physiological functions.
XX The rhesus MC-4R gene was isolated by PCR using a series of four
XX oligonucleotides (AAA26973-A26976) based on the human MC-4R gene sequence
XX and designed to incorporate a restriction enzyme site for cloning into
XX the expression vector pCI-neo. The recombinant vector was transfected
XX into DH5a cells in preparation for DNA sequencing. The present sequence
XX or a mutated form may be introduced into an expression vector for
XX expression in host cells. The subcellular membrane fractions will
XX comprise either wild-type or mutant forms of rhesus MC-4R at enhanced
XX levels and can be used in assays to identify ligand binding, activators
XX and modulators, agonists and antagonists of MC-4R. This will allow for
XX selection of compounds that are active for the rhesus receptor in vitro
XX and will allow the selection of novel drugs to treat obesity.
XX SQ Sequence 1030 BP; 239 A; 254 C; 222 G; 315 T; 0 other;
```

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Query Match 41.2%; Score 817.6; DB 21; Length 1030;
Best Local Similarity 87.4%; Pred. No. 8.8e-184;
Matches 895; Conservative 0; Mismatches 129; Indels 0; Gaps 0;
QY 436 CTTGTTGAGGATGAACATCCACCTTTCAGACGGAATGCACACTTCTCTCCACTTCTGGA 495
Db 6 CTCCTGCCAGCATGGTGAATCCACCCACCGTGGATGCACGCTTCTCTGCACCTCTGGA 65
QY 496 ACCGAGCAGCCTACGGACGACGACGCAACGCACTGAGTCCCTTGGGCAAGAGCTACCCGG 555
Db 66 ACCGAGCAGCAGCAGACTGCACGCAATGCAGTGAAGTCCCTTGGAAAGAGCTACTCTG 125
QY 556 ACGGGGATGTACGAGCAACTTTCGTCCTCCCGGAGGTGTTGCTGACTCTGGGGGTCA 615
Db 126 ATGGAGGTGCTACGAGCAACTTTTGTGCTCTCTCTGAGGTGTTGTGACTCTGGGTGCA 185
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Oy 616 TAAGCTTGCTGGAGAACATTTCTGATGTCGTGCAATAGCCAAAGAACAAAGAAATCTGCAC 675
  ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 186 TCAGCTTGTGGAGAAATATCTAGTGTGTCGCAATAGCCAAAGAACAAAGAAATCTGCAT 245
Oy 676 CACCACATGCTATTTTTCATCTGTCAGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 735
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 246 CACCACATGCTATTTTTCATCTGTCAGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 305
Oy 736 ACCGGTCAGACACCATCTGTCATCACCTGTTGAACAGTACGATACGACGACGACGAGTT 795
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 306 ATGGATCAGAACCATCTGTCATCACCTATTAACAGTACGATACGACGACGAGTT 365
Oy 796 TCACGGTGAATTAATGATAATCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 855
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 366 TCACAGTGAACATTTGATAATGTTATGCTCAGTACGTCGTCGTCGTCGTCGTCGTCGTC 425
Oy 856 TTTGACGCTGCTCTCAATTCAGTGGACAGGTCATCTTATCTTATCTTATCTTATCTTATCT 915
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 426 TTTGACGCTGCTCTCAATTCAGTGGACAGGTCATCTTATCTTATCTTATCTTATCTTATCT 485
Oy 916 ACCATAACATCATGACGGTGGGGTGGGATCATCATCATCATCATCATCATCATCATCATCAT 975
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 486 ACCATAACATCATGACGGTGGGGTGGGATCATCATCATCATCATCATCATCATCATCATCAT 545
Oy 976 GCACGGTGTACAGGATCTTGTTCATCAATTTACTCGGACAGTACCTGCTCATCATCTGCTGCC 1035
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 546 GCACGGTGTACAGGATCTTGTTCATCAATTTACTCGGACAGTACCTGCTCATCATCTGCTGCC 605
Oy 1036 TCATCAGATGTTCTTCCACATGCTGGCCCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1095
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 606 TCATCAGATGTTCTTCCACATGTTGGCTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 665
Oy 1096 TCATGGCCAGACTGCATCAAGAGATCGCGCTCTCCCGGACGCGGACCATCCGCC 1155
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 666 TGATGGCCAGGCTTCACATTAAGAGATGCTGCTCCCGGACGCGGACCATCCGCC 725
Oy 1156 AAGGGCCCAACATGAAGGGTGCCTTACCTTGACCATCTCATTTGGGCTCTTGGCTGCT 1215
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 726 AAGGGCCCAATGAAGGGAGCGATTAATTTGACCATCTCATTTGGGCTCTTGGCTGCT 785
Oy 1216 GCTGGCTCCATCTTCTCCATCTGATATTTCTACATCTCTTTGCTCCCGAGAAATCCATCT 1275
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 786 GCTGGGCCCAATCTTCTCCATCTGATATTTCTACATCTCTTTGCTCCCGAGAAATCCATCT 845
Oy 1276 GTGTGTGCTTCATCTCATCTTAATCTGATCTCACTTCTGATCTGATCTGATCTGATCTGAT 1335
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 846 GTGTGTGCTTCATCTCATCTTAATCTGATCTCACTTCTGATCTGATCTGATCTGATCTGAT 905
Oy 1336 TCGACCTCTCATTTATGCACTCCGGAGCCCAAGAGCTGAGGAAACCTTCAAGAGATCA 1395
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 906 TCGATCTCTGATTTATGCACTCCGGAGTCAAGAACTAAGAAACCTTCAAGAGATCA 965
Oy 1396 TCTGTGTGATATCTTCTGGGTGGCTTTGTGACTTGTCTAGCAGATCTAGCTGGGACAG 1455
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 966 TCTGTGTGATATCTTCTGGGTGGCTTTGTGACTTGTCTAGCAGATCTAGCTGGGACAG 1025
Oy 1456 AGGA 1459
  |||
Db 1026 AGCA 1029
```

RESULT 9

```
AAAT68790
ID AAAT68790 standard; DNA; 996 BP.
XX
XX
AC AC
XX XX
DT DT
XX XX
DE Melanocortin-4 receptor coding sequence.
XX
KW Melanocortin-3; MC3R; MC1R; MC2R; MC4R; MC5R; human; mouse; melanocyte;
```

```
KW pro-opiomelanocortin; adrenal cortical function; behaviour; learning;
KW memory; cardiovascular system; analgesia; thermoregulation; prolactin;
XX neurohumoral agent; biogenic amine; ds.
OS Homo sapiens.
XX
XX US5622860-A.
XX
XX 22-APR-1997.
XX
XX 17-FEB-1994; 94US-0200711.
XX
XX 17-FEB-1994; 94US-0200711.
XX (UNMI ) UNIV MICHIGAN.
XX
XX Gantz I, Yamada T;
XX
XX WPI; 1997-244394/22.
XX P-PSDB; AAW19704.
XX
```

Nucleic acid molecules encoding melanocortin receptors - useful to transfect mammalian cells lacking endogenous receptors to induce their expression

Claim 4; Column 43-46; 58pp; English.

AAAT68789-T68793 represent the coding sequences for human and mouse melanocortin (MC) receptors. This sequence encodes the MC4R, expressed primarily in brain, and is absent in the adrenal cortex, melanocytes and placenta, and is located at chromosome locus 18q21.3. MCs are products of pro-opiomelanocortin post-translational processing, and are known to have a broad array of physiological actions. MCs are known to have effects on adrenal cortical functions and on melanocytes, as well as affecting behaviour, learning, memory, control of the cardiovascular system, analgesia, thermoregulation and the release of other neurohumoral agents (such as prolactin and biogenic amines). The nucleic acids can be used to transfect mammalian cells lacking endogenous MC receptors to induce their expression. These sequences can also be used to screen and identify drugs which specifically react with MCs on the surface of a cell. The drugs can then be used for treating diseases which have MCs implicated as one of their causes. Vectors containing these sequences can also be used to treat the diseases.

Sequence 996 BP; 227 A; 243 C; 213 G; 313 T; 0 other;

Query Match 41.2%; Score 817.4; DB 18; Length 996;
Best Local Similarity 89.3%; Pred. No. 9.6e-184;
Matches 881; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

```
Oy 455 CACCTTCAGCAGCAATGCACACTTCTCTCCACTTCTGGAACCGCAGCAGCTACGGACA 514
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 9 CTCACCCACCGTGGGATGCACACTTCTCTGACCTCTGGAACCGCAGCAGTTACAGACT 68
Oy 515 GCAGCGCAACGCCACTGAGTCCCTTGGCAAAAGGCTACCCCGACGGGATGCTACGAGCA 574
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 69 GCACAGCAATGCCACTGAGTCCCTTGGAAAGGCTACTCTGATGAGGGTCTACGAGCA 128
Oy 575 ACTCTTCGTCCTCCCGGAGGTGTCGTGACTCTCTGGGGGTCTATAAGCTTCTGGGAGAACAT 634
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 129 ACTTTTCTCTCTGAGGTGTTTGTGACTCTCTGGGTGTCATCTGTTGTTGGAGATAT 188
Oy 635 TCTGGTGTCTGGCAATAGCAAGCAAAATCTGCACCTCACCCATCTACTTTTTCAT 694
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 189 CTTAGTGTATGTGGCAATAGCAAGCAAAATCTGCAATTCACCCATCTACTTTTTCAT 248
Oy 695 CTGTAGCCTGCTGTGGCCGATATGCTGCTGAGGCTTTTCCAAACGGCTCAGAGACCATCGT 754
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 249 CTGCAGCTTGGCTGTGATATGCTGCTGAGCGCTTCAATGATGATGATGATGATGAT 308
Oy 755 CATCACCTGTTGAACAGTACGGATACGAGACCGCAGAGTTTCACGGTGAATATTGATAA 814
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 309 CATCACCTATTAACAGTACAGATACGATACGATGACAGAGTTTCACAGTGAATATTGATAA 368
```


Qy	815	TGTCATTGACTCGGTGATCTGTAGCTCCTTGTCTGCGCCTCGATTTGGACGCTGCTCTCAAT	874
Db	369	TGTCATTGACTCGGTGATCTGTAGCTCCTTGTCTGCTGTCATCCATTTGGACGCTGCTCTCAAT	428
Qy	875	TGCAGTGGACAGGTACTTTACTATCTTTTATGCCCTCCACTACCATAACATCATGACGGT	934
Db	429	TGCAGTGGACAGGTACTTTACTATCTTTTATGCCCTCCACTACCATAACATTTATGACAGT	488
Qy	935	GAGCGGGTTGGGATCATCATAGTTGCATCTCTGGGGGCTTGGACGCTGTCAGGCATCTT	994
Db	489	TAAGCGGGTTGGGATCATCATAGTTGTATCTCTGGGAGCTTGCACGGTTTCAGGCATTTT	548
Qy	995	GTTTCATCATTTACTTCGGACAGTACTGCTGTATCATCTGCCTCATCACCATGTTCTTCAC	1054
Db	549	GTTTCATCATTTACTTCAGATAGTAGTGTGCATCATCTGCCTCATCACCATGTTCTTCAC	608
Qy	1055	CATGCTGGCCCTCATGGCTTCTCTCTACGTCCACATGTTTCTCATGGCCAGAGCTGCACAT	1114
Db	609	CATGCTGGCTTCTCATGGCTTCTCTCTATGTCCACATGTTTCTCATGGCCAGGCTTCACAT	668
Qy	1115	CAAGAGAAATCGCGTCTCTCCCGGACCGGCACCATCCGGCCAAAGGGCCCAACATGAAGGG	1174
Db	669	TAAGAGGATTTGCTGTCTCTCCCGGCACTGGTGCATCCCGCAAGGTGCCAATATGAAGGG	728
Qy	1175	TGCATTACCTTGACCATACTCATTTGGGGTCTTCGTCGCTGCTGGGCTCCATTCCTCCT	1234
Db	729	AGCGATTACCTTGACCATCTGATTTGGCGTCTTTGTGTGCTGGGCCCATCTTCCT	788
Qy	1235	CCACTTGATATTTACATCTCTTGTCCCCAGAATCCATACTGTGTGCTTTCATGTCTCA	1294
Db	789	CCACTTAAATTTACATCTCTTGTCTCAGAATCCATATTGTGTGCTTTCATGTCTCA	848
Qy	1295	CTTTAACTTGACTCATTTCTGATCATGTGTAACCTCCATCATCGACCCCTCATTTATGC	1354
Db	849	CTTTAACTTGATCTCATCTACTGATCATGTGTAATTCATATCGATCCTCTGTGTTATGC	908
Qy	1355	ACTCCGGAGCAAGAGCTGAGGAAAACCTTCAAAGAGATCATCTGTTGCTATCCTCTGGG	1414
Db	909	ACTCCGGAGTCAAGAACTGAGGAAAACCTTCAAAGAGATCATCTGTTGCTATCCCTGGG	968
Qy	1415	TGCGCCTTGTGACTTGTCTAGCAGATA	1441
Db	969	AGGCCCTTGTGACTTGTCTAGCAGATA	995
RESULT 10			
AAV62352			
ID	AAV62352 standard; DNA; 996 BP.		
XX	AAV62352;		
AC			
XX			
DT	17-DEC-1998 (first entry)		
XX			
DE	Melanocortin-4 receptor gene.		
XX			
KW	Human melanocortin-4 receptor; MC4; MC1; MC3; therapeutic; brain;		
KW	adrenal cortex; melanocyte; placenta; ss.		
XX			
OS	Homo sapiens.		
XX			
FH	Key		
FT	Location/Qualifiers		
FT	1..996		
FT	/*tag= a		
FT	/product= "MC4"		
FT	/note= "No stop codon given"		
XX			
PN	US5817787-A.		
XX			
XX	06-OCT-1998.		
XX			
XX	23-APR-1997; 97US-0842045.		
XX			

PR	17-FEB-1994;	94US-0200711.	
PR	27-JUN-1996;	96US-0672109.	
PR	23-APR-1997;	97US-0842045.	
XX		(UNMI) UNIV MICHIGAN.	
PA			
XX	Gantz I, Yamada T;		
FI			
XX	WPI; 1998-556471/47.		
DR	P-PSDB; AAW79687.		
DR			
XX			
PT	DNA encoding melanocortin-5 receptor - useful in hybridisation		
PT	assays for melanocortin-5 receptor nucleic acids		
XX			
PS	Disclosure; Column 43-46; 58pp; English.		
XX			
CC	The present sequence represents the nucleic acid of the gene encoding the		
CC	human melanocortin-4 (MC4) receptor, localised to chromosome 18q21.3.		
CC	This receptor is activated by both the amino and carboxyl terminal end		
CC	of melanocortins and has been found to be expressed primarily		
CC	in the brain and is absent from the adrenal cortex, melanocytes and		
CC	placenta. This sequence was identified by using oligonucleotides		
CC	constructed from previously identified receptors MC1 and MC3, this was		
CC	performed by using these oligonucleotides to search genomic DNA for other		
CC	members of the receptor family. These genes and their products may be		
CC	used to provide therapeutic vehicles for the treatment of processes		
CC	involving the function of melanocortin receptors.		
XX			
SQ	Sequence 996 BP; 227 A; 243 C; 213 G; 313 T; 0 other;		
	Query Match 41.2%; Score 817.4; DB 19; Length 996;		
	Best Local Similarity 89.3%; Pred. No. 9,6e-184;		
	Matches 881; Conservative 0; Mismatches 106; Indels 0; Gaps 0;		
QY	455 CACCCCTTACACGGGAATGCACACTTCTCTCCACTTCTTGGAAACCGCAGCACCTACGGACA	514	
Db			
	9 CTCACCCACCGTGGGATGCACACTTCTCTGCACCTCTGGAAACCGCAGCAGTTACAGACT	68	
QY	515 GCACGGCAGCGCACATGAGTCCCTTGGCAAGGCTACCCGACGGGGATGCTACGAGCA	574	
Db			
	69 GCACGAGATGCCAGTGAGTCCCTTGGAAAGGCTACTCTGATGGAGGGTGCTACGAGCA	128	
QY	575 ACTCTTGTGCTCCCCGGAGGTGTCTGTGACTCTGGGGGTGCATTAAGCTTGCTGGAGAACAT	634	
Db			
	129 ACTTTTGTCTCTCTGAGGTGTGTGTGACTCTGGGTCTCATCAGCTTGTGTGGAGAATAT	188	
QY	635 TCTGGTGATCGTGGCAATAGCCAAAGACAGAAATCTGCACCTACCCATGTACTTTTTCAT	694	
Db			
	189 CTTAGTGATGTGGCAATAGCCAAAGACAGAAATCTGCATTCACCATGTACTTTTTCAT	248	
QY	695 CTGTAGCCTGGCTGTGGCCCATATGCTGGTGTAGCGTTTCCAAACGGGTTCAGAGACCATCGT	754	
Db			
	249 CTCAGCTTGGCTGTGGCTGATATGCTGGTGTAGCGTTTCCAATGGATCAGAAACCATAT	308	
QY	755 CATCACCTGTTGAACAGATACGGATACGGACGGCAGAGTTTCCACGGTGAATATTGATAA	814	
Db			
	309 CATCACCTATTAAACAGTACAGATACGGATGCACAGAGTTTCCACAGTGAATATTGATAA	368	
QY	815 TGTCAATGACTCGGTGATCTGTAGCTCCTTGCTCGCCTCGATTTTGACGGCTGCTCTCAAT	874	
Db			
	369 TGTCAATGACTCGGTGATCTGTAGCTCCTTGCTCGCCTCGATTTTGACGGCTGCTCTCAAT	428	
QY	875 TGCAGTGGACAGGTACTTACTACTTCTTTATGCCCTCCAGTACCATAAATCATATGACGGT	934	
Db			
	429 TGCAGTGGACAGGTACTTACTACTTCTTATGCTCTCCAGTACCATAAATATGACAGT	488	
QY	935 GAGCCGGGTGGGATCATCATGATTCATCTCGGGCGGCTTGCACGGTGTCCAGGCATCTT	994	
Db			
	489 TAAGCCGGGTGGGATCATCATGATTCATCTCGGGCAGCTTGCACGGTGTCCAGGCATCTT	548	
QY	995 GTTCATCATTTACTCCGACAGTACTGCTGTCACTCATCTGCCTCATCACCATGTTCTTCAC	1054	
Db			
	549 GTTCATCATTTACTCCGACAGTACTGCTGTCACTCATCTGCCTCATCACCATGTTCTTCAC	608	


```
QY 1055 CATGCTGGCCCTCATGGCTTCTCTAGTCCACATGTTCTCATGGCCAGACTGCACAT 1114
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 609 CATGCTGGCTCTCATGGCTTCTCTATGATCCACATGTTCTGATGGCCAGGCTTCAT 668
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1115 CAAGAGAAATCCGCTCTCCGGGACCGGACCATCGCCCAAGGGCCAAACATGAAGG 1174
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 669 TAAGAGGATGCTGCTCTCCCGGCACTGGTGCCATCCGCCAAGGTGCCAATGAAGG 728
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1175 TGCCATTACCTTGACCATACATGTTGGGCTTCTGCTGCTGCTGGGCTCCATCTTCCT 1234
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 729 AGCGATTACCTTGACCATCTGATGGGCTTCTTGTGCTGCTGGGCCCATCTTCCT 788
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1235 CCACCTTGATATTACATCTCTTGTCCCGAGATCCACATCTGTTGCTTCATGTCFCA 1294
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 789 CCACCTTAATATTACATCTCTTGTCTCAGAACCATATGTTGTTGCTTCATGTCFCA 848
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1295 CTTTAACTTGATCTCATCTGATGATGATGATGATGATGATGATGATGATGATGAT 1354
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 849 CTTTAACTTGATCTCATCTGATGATGATGATGATGATGATGATGATGATGATGAT 908
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1355 ACTCCGAGCAAGAGCTGAGAAACCTTCAAGAGATCATCTGTTGCTATCCCTGGG 1414
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 909 ACTCCGAGCTCAAGACTGAGAAACCTTCAAGAGATCATCTGTTGCTATCCCTGGG 968
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1415 TGGCCTTTGTGACTTGTCTAGCAGATA 1441
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 969 AGGCTTTGTGACTTGTCTAGCAGATA 995
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
AAV06400
ID AAV06400 standard; DNA; 996 BP.
XX AC AAV06400;
XX DT 30-APR-1998 (first entry)
XX DE Human melanocortin-4 (MC4) receptor encoding DNA.
XX KW Melanocortin receptor; ligand; MC4; human; ds.
XX OS Homo sapiens.
XX FT Key
XX FT CDS
XX FT Location/Qualifiers
XX FT 1..996
XX FT /*tag= a
XX FT /product= melanocortin-4 receptor
XX FT /note= "stop codon is not indicated"
XX PN US5703220-A.
XX PD 30-DEC-1997.
XX PF 27-JUN-1996; 96US-0671525.
XX PR 17-FEB-1994; 94US-0200711.
XX PR 27-JUN-1996; 96US-0671525.
XX PA (UNMI ) UNIV MICHIGAN.
XX PI Gantz I, Yamada T;
XX PI WPI; 1998-076484/07.
XX DR P-PSDB; AAW33724.
XX PT DNA encoding human melanocortin-4 receptor - and cells useful in
XX PT assay for MC4 receptor ligands
XX PS Claim 7; Columns 43-46; 59pp; English.
XX CC This DNA encodes a human melanocortin receptor-4 (MC4). The MC4 receptor
XX CC of this invention is activated by amino acids in the carboxyl and amino
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CC terminal portions of the heptapeptide sequence shared by all the
CC melanocortin peptides. MC4 is expressed primarily in brain and is notably
CC absent in the adrenal cortex, melanocytes and placenta. The MC4 receptor
CC gene was localised to chromosome loci 18q21.3. The invention provides
CC methods to identify ligands that bind to MC4 receptor.
XX
SQ Sequence 996 BP; 227 A; 243 C; 213 G; 313 T; 0 other;
    Query Match 41.2%; Score 817.4; DB 19; Length 996;
    Best Local Similarity 89.3%; Pred. No. 9.6e-184;
    Matches 881; Conservative 0; Mismatches 106; Indels 0; Gaps 0;
QY 455 CACCTTTTCAGCAGCGAATGACACTTCTCTCCACTTCTGGAACCGCAGCACCTAGGACA 514
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 9 CTTCCACCACCGTGGGATGCACACTTCTCTGCACCTCTGGAACCGCAGCAGTTACAGACT 68
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 515 GCACGGCAACGCCACTGAGTCCCTTGGCAAGGCTACCCCGACGGGGATGCTAGGACA 574
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 69 GCACAGCAATCCAGTGGGATGCACACTTCTCTGCACCTCTGGAACCGCAGCAGTTACAGACA 128
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 575 ACTCTTGTCTCCCGGAGGTGTTGCTGACTCTGGGGTCTATAAGCTTGTGGAGAATAT 634
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 129 ACTTTTGTCTCTCTGAGGTGTTGACTCTGGGTGCTATCAGCTTGTGGAGAATAT 188
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 635 TCTGCTGATCTGTCGCAATAGCAAGAACTCTGCACCTCACCCATGTACTTTTCAT 694
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 189 CTTAGTGATTTGGCAATAGCAAGAACTCTGCATTCACCCATGTACTTTTCAT 248
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 695 CTGTAGCCTGTGCGCGATATGCTGGTGAGCGTTTCCACGGGTGAGAGACCATCGT 754
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 249 CTGCAGCTTGGCTGTGCTGATATGCTGGTGAGCGTTTCAAATGATCAGAAACCATAT 308
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 755 CATCACCTTGTGAACAGTACGAGTACGAGCGCAGAGTTTCACGGTGAATATTGATAA 814
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 309 CATCACCTTATAAACAGTACAGATACGAGTTTCACAGTTCAGTAATATTGATAA 368
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 815 TGTCAATTGACTCGGTGATCTGTAGCTCTTCTGCTGCTCTGATTTTGCACCTGCTCTCAAT 874
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 369 TGTCAATTGACTCGGTGATCTGTAGCTCTTCTGCTGCTCTGATTTTGCACCTGCTCTCAAT 428
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 875 TGCAGTGGACAGGTACTTTACTATCTTTTATGCCCCCTCCAGTACCACATCATGACGGT 934
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 429 TGCAGTGGACAGGTACTTTACTATCTTCTATGCTCTCCAGTACCACATCATGACAGT 488
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 935 GAGCGGGTTGGGATCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 994
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 489 TAAGCGGGTTGGGATCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 548
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 995 GTTCATCATTTTACTCGGACAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1054
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 549 GTTCATCATTTTACTCGGACAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1055 CATGCTGGCCCTCATGGCTTCTCTCTAGTCCACATGTTCTCATGGCCAGACTGCACAT 1114
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 609 CATGCTGGCTCTCATGGCTTCTCTCTATGATCCACATGTTCTGATGGCCAGGCTTCAT 668
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1115 CAAGAGAAATCCGCTCTCCGGGACCGGACCATCGCCCAAGGGCCAAACATGAAGG 1174
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 669 TAAGAGGATGCTGCTCTCCCGGCACTGGTGCCATCCGCCAAGGTGCCAATGAAGG 728
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1175 TGCCATTACCTTGACCATACATGTTGGGCTTCTGCTGCTGCTGGGCTCCATCTTCCT 1234
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 729 AGCGATTACCTTGACCATCTGATGGGCTTCTTGTGCTGCTGGGCCCATCTTCCT 788
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1235 CCACCTTGATATTACATCTCTTGTCCCGAGATCCACATCTGTTGCTTCATGTCFCA 1294
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 789 CCACCTTAATATTACATCTCTTGTCTCAGAACCATATGTTGTTGCTTCATGTCFCA 848
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1295 CTTTAACTTGATCTCATCTGATGATGATGATGATGATGATGATGATGATGATGAT 1354
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 849 CTTTAACTTGATCTCATCTGATGATGATGATGATGATGATGATGATGATGATGAT 908
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1355 ACTCCGAGCAAGAGCTGAGAAACCTTCAAGAGATCATCTGTTGCTATCCCTGGG 1414
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

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Db 909 ACTCCGGAGTCAAGAACTGAGGAAACCTTCAAGAGATCATCTGTTGCTATCCCTGGG 968
1415 TGGCCTTTGAGCTTGTCTAGCAGATA 1441
Db 969 AGGCCTTTGAGCTTGTCTAGCAGATA 995

RESULT 12
AAAX01964
ID AAX01964 standard; DNA; 996 BP.
XX AAX01964;
XX 21-APR-1999 (first entry)
XX Human MC4 DNA.
DE
XX Melanocortin-4 receptor; MC1; MC2; MC3; MC4; MC5; detection; probe;
KW receptor binding; secondary signalling; tissue distribution; ds.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..996
FT FT /*tag= a
FT FT /product= "MC4"
FT FT /note= "partial sequence, no stop codon given"
XX
XX US5869257-A.
XX
XX 09-FEB-1999.
XX 23-APR-1997; 97US-0842238.
XX
XX 17-FEB-1994; 94US-0200711.
XX 27-JUN-1996; 96US-0671525.
XX 23-APR-1997; 97US-0842238.
XX
XX (UNMI ) UNIV MICHIGAN.
XX
XX Gantz I, Yamada T;
XX
XX WPI; 1999-152760/13.
XX P-PSDB; AAW92442.
XX
XX Probe for detecting melanocortin-4 receptor genes - that
XX Specifically hybridises to defined DNA sequence
XX
XX Example 1; Column 43-46; 60pp; English.
XX
XX This sequence encodes the human melanocortin-4 receptor, MC4. This
XX protein is used in a method in which a nucleic acid probe useful for
XX specifically detecting melanocortin-4 receptor genes is described.
XX This probe is used to isolate genes encoding melanocortin receptors,
XX to characterise melanocortin receptor binding and secondary signalling
XX and to determine tissue distribution of the melanocortin receptors.
XX
XX Sequence 996 BP; 227 A; 243 C; 213 G; 313 T; 0 other;

Query Match 41.2%; Score 817.4; DB 20; Length 996;
Best Local Similarity 89.3%; Pred. No. 9.6e-184;
Matches 881; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 455 CACCCTTCAGCAGGAAATGCACACTCTCTCCACTTCTGGAACCGCAGCACCTACGGACA 514
Db 9 CTCCACCCACCGTGGGATGCACACTCTCTGCACCTCTGGAACCGCAGCAGTTACAGACT 68
QY 515 GCACGGAACCGCACTGAGTCCCTTGGCAAGGCTACCCGACGGGATGCTACGAGCA 574
Db 69 GCACAGCAATGCCAGTGAAGTCCCTTGGAAAGGCTACTCTGATGAGGGTGTCTAGCAGCA 128
QY 575 ACTCTTCGTCTCCCGGAGGTGTTCTGCTGACTCTGGGGTTCATPAAGCTTGTCTGGGAACAT 634
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Db 129 ACTTTTGTCTCTCCTCCTGAGGTGTTGTGACTCTGGGTGTCATCAGCTTGTGGAGAATAT 188
QY 635 TCTGGTGATCGTGGCAATAGCCAAAGAAATCTGCACCTACCCCATGTACTTTTCAT 694
Db 189 CTTAGTGAATTTGGCAATAGCCAAAGAAATCTGCAATCTACCCATGTACTTTTCAT 248
QY 695 CTGTAGCCTGGCTGTGGCCGATATGCTGTGAGCGTTTCCAAACGGGTCCAGAGACCATCGT 754
Db 249 CTGCAGCTTGGCTGTGGCTGATATGCTGGTGAGCGTTTCAATGGATCAGAAACCAATAT 308
QY 755 CATCACCTTGTGAACAGTACGGATACGGACGGCAGAGTTTACCGGTGAATATTGATAA 814
Db 309 CATCACCTTATTAACAGTACAGATACGGATGCACAGAGTTTCCACAGTGAATATTGATAA 368
QY 815 TGTCAATTGACTCGGTGATCTGTAGTCCCTTGTGCGCTCGATTTGAGCGCTGCTCTCAAT 874
Db 369 TGTCAATTGACTCGGTGATCTGTAGTCCCTTGTGCGCTCGATTTGAGCGCTGCTCTCAAT 428
QY 875 TGCAGTGGACAGTACTTTTACTATCTTTTATGCCCTCCAGTACCATTAACATCATGACGT 934
Db 429 TGCAGTGGACAGTACTTTTACTATCTTTCTATGCTCTCCAGTACCATAATATGACAGT 488
QY 935 GAGCGGGTTGGGATCATCATCAGTTGCTGTGGCGGCTTGCACGGTGTACAGGCACTTT 994
Db 489 TAAGCGGGTTGGGATCATCATTAAGTTGTATCTGGGCAGCTTGCACGGTTTCAGGCAATTT 548
QY 995 GTTCATCATTTACTCGGACAGTACTGCTGTCTCATCTGCTCCCTCATCACCATGTTCTTCA 1054
Db 549 GTTCATCATTTACTCAGATAGTAGTCTGTCTCATCTGCTCCCTCATCACCATGTTCTTCA 608
QY 1055 CATGTGGCCCTCATGGCTTCTCTTACCTGCACATGTTTCCCTCATGGCCAGACTGCACAT 1114
Db 609 CATGTGGCTCTCATGGCTTCTCTTATGTCACATGTTTCCCTCATGGCCAGCTTCACAT 668
QY 1115 CAAGAGAAATCGCGCTCTCTCCCGGCAACCGGCAACCATGCGCCCAAGGGGCCAACATGAAGG 1174
Db 669 TAAGAGGATTTGCTCTCTCCCGGCACTGGTGCATCCGCAAGGTGCCAATATGAAGG 728
QY 1175 TGCATTACCTTGACCACTACTCATTTGGGGTCTTCGCTGCTGCTGGGTCCATTTCTCT 1234
Db 729 AGCGATTACCTTGACCACTCTGATTGGCGCTTTTGTGCTGCTGGGCCCATTTCTCTCT 788
QY 1235 CCACCTTGATATTCTATCATCTCTGTCCCGCAAGATCCATCTGCTGTGCTCATGTCTCA 1294
Db 789 CCACCTTAATATTCTACATCTCTGTCCCTCAGAAATCCATATTGTGTGCTCATGTCTCA 848
QY 1295 CTTTAACCTTGTACCTTCTCATCTGATCATGTGTAACCTCCATFATCGACCCCTCTCATTTATGC 1354
Db 849 CTTTAACCTTGTATCTCATACTCATCATGTGTAATCAATCATCGATCCCTCTGATTATGC 908
QY 1355 ACTCCGGAGCCAAAGAGTGGAGAAACCTTCAAGAGATCATCTGTTGCTATCTCTCTGGG 1414
Db 909 ACTCCGGAGTCAAGAACTTGAAGAAACCTTCAAGAGATCATCTGTTGCTATCCCTCTGGG 968
QY 1415 TGGCCTTTGAGCTTGTCTAGCAGATA 1441
Db 969 AGGCCTTTGAGCTTGTCTAGCAGATA 995

RESULT 13
AAAX75829
ID AAX75829 standard; DNA; 996 BP.
XX AAX75829;
XX 22-JAN-2001 (first entry)
XX
XX DNA encoding a human melanocortin-4 receptor polypeptide.
DE
XX Human; melanocortin-1 receptor; melanocortin-2 receptor; 16q24.3;
KW 18p11.2; melanocortin-3 receptor; 20q13.2; melanocortin-4 receptor;
KW 18q21.3; melanocortin; ds.
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PR 26-FEB-1999; 9905-0121852.
PR 12-MAR-1999; 9905-0123944.
PR 12-MAR-1999; 9905-0123945.
PR 12-MAR-1999; 9905-0123946.
PR 12-MAR-1999; 9905-0123948.
PR 12-MAR-1999; 9905-0123949.
PR 12-MAR-1999; 9905-0123951.
PR 28-MAY-1999; 9905-0136436.
PR 28-MAY-1999; 9905-0136437.
PR 28-MAY-1999; 9905-0136439.
PR 28-MAY-1999; 9905-0137127.
PR 28-MAY-1999; 9905-0137131.
PR 28-MAY-1999; 9905-0137567.
PR 30-JUN-1999; 9905-0141448.
PR 27-AUG-1999; 9905-0151114.
PR 03-SEP-1999; 9905-0152524.
PR 28-SEP-1999; 9905-0156633.
PR 29-SEP-1999; 9905-0156655.
PR 29-SEP-1999; 9905-0156634.
XX
PA (AREN-) ARENA PHARM INC.
XX
XX Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;
PI Gore M, Liaw CW, Lin I, Lowitz K, White C;
XX
XX WPI: 2000-317986/27.
DR P-PSDB; AAB02845.
XX
XX Non-endogenous, human G protein-coupled receptors for screening
PT receptor, inverse or partial agonists useful as therapeutic agents -
XX
XX Example 1; Page 132-133; 187pp; English.
XX
XX The present invention describes transmembrane receptors, preferably
CC human G protein coupled receptors (GPCR), for which the endogenous
CC ligand is unknown (orphan GPCR receptors). More specifically the present
CC invention relates to non-endogenous, constitutively activated versions
CC of a human GPCR. These non-endogenous human GPCRs can be useful for
CC the direct identification of candidate compounds as receptors agonists,
CC inverse agonists or partial agonists for use as pharmaceutical agents.
CC AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
CC the exemplification of the present invention.
XX
XX Sequence 999 BP; 229 A; 243 C; 214 G; 313 T; 0 other;
SQ
Query Match 41.2%; Score 817.2; DB 21; Length 999;
Best Local Similarity 89.1%; Pred. No. 1.1e-183;
Matches 882; Conservative 0; Mismatches 108; Indels 0; Gaps 0;
QY 455 CACCCCTTCAGCAGGGAATGCACACTTCTCTCCACTTCTGGAAACCGCAGCACCTACGGACA 514
Db 9 CTCACCCACCGTGGGATGCACACTTCTCTGACCTCTGGAACCGCAGCTTACAGACT 68
QY 515 GCACGGCAACGCCACTGCTCCCTTGGCAAGGCTACCCCGAGGGGGATGCTACGAGCA 574
Db 69 GCACAGCAATGCAGTGAGTCCCTTGGAAAGGCTACTCTGATGGAGGGTGTACGAGCA 128
QY 575 ACTCTTCGCTCCCGGAGGTGTCGTGACTCTGGGGGTCAATAAGCTTCTGGAGAACAT 634
Db 129 ACTTTTGTCTCTCGTGGGTGTTGTGACTCTGGGTGTCATCAGCTTGTGGAGAAATAT 188
QY 635 TCTGGTGATGCTGGCAATAGCAAGAACAAAGAAATCTGCACCTACCCCATGACTTTTTCAT 694
Db 189 CTAGTGTATGTGGCAATAGCAAGAACAAAGAAATCTGCATTCACCCATGACTTTTTCAT 248
QY 695 CTGTAGCCCTGGCTGTGGCCGATATGCTGTGAGCGTTTCCACGGGTACAGACCATCGT 754
Db 249 CTGACGCTGGCTGTGGCTGTATGCTGTGAGCGTTTCAATGATATCAGAACCATAT 308
QY 755 CATCACCCCTGTTGAACAGTACCGGATACGGACGCGAGAGTTCACGGTGAATATTGATAA 814
Db 309 CATCACCCCTATTAAACAGTACAGATACGGATGCACAGAGTTTCACAGTGAATATTGATAA 368

QY 815 TGTCAATTGACTCGGTGATCTGTAGCTCTTGTCTGCGCTCGAATTTGAGCCTGCTCTCAAT 874
Db 369 TGTCAATTGACTCGGTGATCTGTAGCTCTTGTCTGCGCTCGAATTTGAGCCTGCTCTCAAT 428
QY 875 TGCAGTGGACAGGTACTTTTACTATCTTTTATGCCCTCCAGTACCATAACATCATGACGTT 934
Db 429 TGCAGTGGACAGGTACTTTTACTATCTTTTATGCCCTCCAGTACCATAACATCATGACGTT 488
QY 935 GAGGCGGGTTGGGATCATCATCAGTTGTCATCTGGGGGGTTCGACAGGTTGTCAGGCACTTT 994
Db 489 TAAGCGGGTTGGGATCAGCATAGTTGTATCTGGGCGAGCTTGCACGGTTTCAGGCACTTT 548
QY 995 GTTCATCATTTTACTCGGACAGTACTGCTGTCAATCATCTGCCCTCATCACCATGTTCTTCAC 1054
Db 549 GTTCATCATTTTACTCGGACAGTACTGCTGTCAATCATCTGCCCTCATCACCATGTTCTTCAC 608
QY 1055 CATGCTGGCCCTCATGCGCTTCTCTCTACGTCACATGTTCTCTCATGCGGCGAGTGCACAT 1114
Db 609 CATGCTGGCTCTCATGCGCTTCTCTCTATGTCCACATGTTCTCTCATGCGGCGAGTGCACAT 668
QY 1115 CAAGGAATCGCGTCTCTCCGGGACCGCACCATCCGCAAGGGGCCCAACATGAAGG 1174
Db 669 TAAGAGGATGTGCTCTCTCCGGGACTGTGCGCATCCCGCAGGTGCCAATATGAAGG 728
QY 1175 TGCCATTACTTTGACCATACTCATTTGGGGTCTTCTGCTGCTGCTGGGCTTCCATTTCTCT 1234
Db 729 AGCGATTACTTTGACCATCTCATTTGGCGCTTTTGTGCTGCTGGGCGCCCATTTCTCT 788
QY 1235 CCACCTTGATTTCTACATCTCTTGTCCCGCAGAAATCCATGCTGCTGCTTCTCATGCTCA 1294
Db 789 CCACCTTAATTTCTACATCTCTTGTCTCAGAAATCCATATTTGCTGCTGCTGCTGCTCA 848
QY 1295 CTTTAACTTGTACCTCATTTCTCATGCTGTAACCTCATCATCGACCCCTCATTTATGC 1354
Db 849 CTTTAACTTGTATCTCATCTCATGCTGTAATTCATCATGATCTCTCATTTATGC 908
QY 1355 ACTCGGGAGCCAGAGCTGAGGAAACCTTCAAGAGATCATCTGTTGCTATCTCTCTGGG 1414
Db 909 ACTCGGGAGCTCAAGAACTGAGGAAACCTTCAAGAGATCATCTGTTGCTATCCCTCTGG 968
QY 1415 TGGCCTTTGTGACTTGTCTAGCAGATACATA 1444
Db 969 AGGCGCTTTGTGACTTGTCTAGCAGATATTA 998
RESULT 15
AAD25897 standard: cDNA; 999 BP.
XX AAD25897;
AC AAD25897;
XX
XX 26-MAR-2002 (first entry)
XX Human melanocortin 4-receptor (MC4R) cDNA.
XX
XX Human; single nucleotide polymorphism; SNP; melanocortin 4-receptor;
KW MC4R; haplotype; obesity; screening; allele-specific oligonucleotide;
KW ASO; gene therapy; anorectic; chromosome 18q22; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH variation replace (307, G)
FT /*tag= a
FT /*standard_name= "Single nucleotide polymorphism"
FT variation replace (527, T)
FT /*tag= b
FT /*standard_name= "Single nucleotide polymorphism"
FT variation replace (594, T)
FT /*tag= c
FT /*standard_name= "Single nucleotide polymorphism"
FT variation replace (606, A)
FT /*tag= d

```
FT      /standard_name= "single nucleotide polymorphism"
FT      replace (751, C)
FT      /*tag= e
XX      /standard_name= "Single nucleotide polymorphism"
PN      WO200179222-A2.
XX      25-OCT-2001.
XX      12-APR-2001; 2001WO-US11943.
XX      12-APR-2000; 2000US-196677P.
XX      (GENA-) GENAISSANCE PHARM INC.
XX      Bentivegna SC, Choi JV, Kazemi A, Lee HH, Nandabalan K, Parks KE;
PI      Sausker EA;
XX      WPI; 2002-082744/11.
DR      P-PSDB; AAE15746.
XX      Novel polymorphic variants of melanocortin 4-receptor gene useful in
PT      studying expression and function of the protein, useful for screening
PT      candidate drugs to treat diseases related to the protein activity e.g.
PT      obesity
XX      Claim 24; Fig 2; 53pp; English.
XX      The invention relates to single nucleotide polymorphisms (SNP) in human
CC      melanocortin 4-receptor (MC4R) gene. MC4R gene haplotypes are useful
CC      for improving the efficiency and reliability of several steps in the
CC      discovery and development of drugs for treating diseases associated
CC      with MC4R activity, e.g. obesity. MC4R gene is useful in studying the
CC      expression and function of MC4R and in expressing MC4R protein for
CC      use in screening for candidate drugs to treat diseases related to
CC      MC4R activity and in studying the effect of the variation on the
CC      biological activity of MC4R as well as on the binding affinity of
CC      candidate drugs targeting MC4R for the treatment of obesity. MC4R
CC      antibody is useful in a variety of diagnostic and prognostic formats
CC      and in therapeutic methods. Allele-specific oligonucleotide (ASO) is
CC      useful as probes and primers, and for assaying a polymorphism in
CC      MC4R gene. MC4R DNA is used in gene therapy. The present sequence is
CC      human MC4R cDNA. MC4R gene is located on chromosome 18q22.
XX      Sequence 999 BP; 229 A; 243 C; 214 G; 313 T; 0 other;
XX      Query Match      41.2%; Score 817.2; DB 24; Length 999;
XX      Best Local Similarity 89.1%; Pred. No. 1.le-183;
XX      Matches 882; Conservative 0; Mismatches 108; Indels 0; Gaps 0;
XX      455 CACGCTTCAGCAGCAGGATGACACTTCTCTCCACTTCTGGAAACCGCAGCAGCTACGGACA 514
XX      9 CTCACCCACCGTGGGATGCACACTTCTCTGCACCTCTGGAAACCGCAGCAGTTACAGACT 68
XX      515 GCACGGCAACGCCACTAGTCCCTTGGCAAAAGGCTACCCGACGGGGGATGCTACGAGCA 574
XX      69 GCACAGCAATGCCAGTGAGTCCCTTGGAAAGGCTACTCTGATGGAGGGTCTACGAGCA 128
XX      575 ACTCTTGCTCTCCCGGAGGTGTTGCTGACTCTGGGGTCTAAGCTTGTGGAGAACAT 634
XX      129 ACTTTTGTCTCTCTGAGGTGTTTGTGACTCTGGGTGTCATCAGCTTGTGGAGAAAT 188
XX      635 TCTGGTGATCGTGCAATAGCAAGAACAAAGAACTGCACCTCACCCATGACTTTTTCAT 694
XX      189 CTTAGTAGTTGGCAATAGCCAAAGAACAAAGAACTGCATTCACCCATGACTTTTTCAT 248
XX      695 CTGTAGCTGCTGTGGCCGATATGCTGGTGAGCGTTTCCAAACGGGTACAGAGACCATCGT 754
XX      249 CTGCAGCTTGGCTGTGCTGATATGCTGGTGAGCGTTTCAATGGATGACAGAACCATAT 308
XX      755 CATCACCCCTGTTGAACAGTAGCGATACGGAGCGCCGACAGTTTTCACGTTGAATATGATAA 814
XX      309 CATCACCCCTATTAAACAGTAGAGATACGGATACGGATGACAGAGTTTTCACAGTGAATATGATAA 368
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Qy      815 TGTCAATTCACGTCGGTGATCTGTAGCTCTCTGCTGCGCTCGATTTCGACGCTGCTCTCAAT 874
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Qy      875 TGCAGTGGACAGGTAAGTCTTACTATCTTTTATGCGCTCCAGTACCATACATGACGGT 934
Db      429 TGCAGTGGACAGGTAAGTCTTACTATCTTATGCTCTCCAGTACCATACATGACAGT 488
Qy      935 GAGCGGGTGGGATCATCATCATCTGCGGCGCTTGCAGGCTGTCAGGATCTT 994
Db      489 TAAGCGGGTGGGATCAGCATAGTGTATCTGGGACGCTTGCAGGCTTTCAGGATTTT 548
Qy      995 GTTCATCATTTTACTCGGACAGTACTGCTGTCTCATCTGCTCATCATCATCATCATCATCAT 1054
Db      549 GTTCATCATTTTACTCAGATAGTGTCTGTCTCATCATCATCATCATCATCATCATCATCAT 608
Qy      1055 CATGCTGGCCCTCATGCTTCTCTCTACGTCCACATGTTCTCATGCGCAGACATGACAT 1114
Db      609 CATGCTGGCTCTCATGCTTCTCTCTATGTCACATGTTCTCTGATGGCCAGGCTTCAT 668
Qy      1115 CAAGAGATCCCGCTCTCCCGGCGCAGCACCACCGCCCAAGGGGCCAACATGAAGGG 1174
Db      669 TAAGAGGATGCTGTCTCTCCCGGCGACTGGTGCCCATCCGCAAGGTGCCAATATGAAGGG 728
Qy      1175 TGCCATTACCTTGACCATACTCATTTGGGGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1234
Db      729 AGCATATACCTTGACCATCTCTGATTTGGGCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCT 788
Qy      1235 CCACCTTGATATTTACATCTCTTGTCCCGCAGAAATCCATCATGCTGTGCTGCTGCTGCTGCTCA 1294
Db      789 CCACCTTAATATTTACATCTCTTGTCCCTCAGAAATCCATATGTTGTGCTGCTGCTGCTGCTCA 848
Qy      1295 CTTTAACTTGTACCTCATCTCTGATCATGCTGTAACCTCCATCATCGACCTCTCATTTATGC 1354
Db      849 CTTTAACTTGTATCTCATACTGATCATGTGTAATTCATCATCTCTGATTTATGC 908
Qy      1355 ACTCCGGAGCAAGAGCTGAGGAAACCTTCAAAGAGATCATCTCTGCTGCTGCTGCTGCTGCT 1414
Db      909 ACTCCGGAGTCAAGAACTGAGGAAACCTTCAAAGAGATCATCTCTGCTGCTGCTGCTGCTGCT 968
Qy      1415 TGGCCTTTGTGACTTGTCTAGCAGATACTA 1444
Db      969 AGGCTTTGTGACTTGTCTAGCAGATATTA 998
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 4, 2003, 18:03:31 ; Search time 51 seconds
(without alignments)
867.435 Million cell updates/sec

Title: US-09-884-211a-4

Perfect score: 1726

Sequence: 1 MNSTLQHGHTSLHFWNRST.....FKETICYPGLGLDLSSRY 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1726	100.0	332	AAU76428	Canine melanocortin
2	1685	97.6	332	AAU76427	Feline melanocortin
3	1638.5	94.9	332	AAW19704	Melanocortin-4 rec
4	1638.5	94.9	332	AAW79687	Melanocortin-4 rec
5	1638.5	94.9	332	AAW33724	Human melanocortin
6	1638.5	94.9	332	AAW92442	Human MC4 protein.
7	1638.5	94.9	332	AAW18769	A human melanocortin
8	1638.5	94.9	332	AAW83185	Synthetic labeled
9	1638.5	94.9	332	AAW68490	Amino acid sequenc
10	1632.5	94.6	332	AAW02845	Human G protein co

11	1632.5	94.6	332	AAE15746	Human melanocortin
12	1627.5	94.3	332	AAW02857	Human G protein co
13	1624.5	94.1	332	AAV94301	Rhesus monkey mela
14	1615.5	93.6	332	AAW83182	Melanocortin recep
15	1596.5	92.5	332	AAW87415	Melanocortin-4 rec
16	1592.5	92.3	332	AAW7831	Human melanocortin
17	1592.5	92.3	332	AAW42377	Homo sapiens mutan
18	1592.5	92.3	332	AAW87869	Human melanocortin
19	1590.5	92.1	332	AAW42378	Homo sapiens mutan
20	1593.5	91.7	332	AAW42379	Homo sapiens mutan
21	1463	84.8	311	AAU08750	Human melanocortin
22	1405	81.4	293	AAW83184	Melanocortin recep
23	1262	73.1	248	AAW78931	Porcine melanocort
24	1257	72.8	248	AAU08751	Porcine melanocort
25	1246	72.2	248	AAW78932	Porcine melanocort
26	1041	60.3	325	AAW79501	Rat melanocortin r
27	1026.5	59.5	325	AAW37833	Mouse melanocortin
28	1026.5	59.5	325	AAW87870	Mouse melanocortin
29	1025.5	59.4	325	AAW94266	Rhesus monkey mela
30	1023.5	59.3	325	AAW19705	Melanocortin-5 rec
31	1023.5	59.3	325	AAW79688	Melanocortin-5 rec
32	1023.5	59.3	325	AAW41067	Mouse melanocortin
33	1023.5	59.3	325	AAW33725	Mouse melanocortin
34	1023.5	59.3	325	AAW92443	Mouse MC5 protein.
35	1023.5	59.3	325	AAW18770	A human melanocort
36	1022.5	59.2	325	AAW79502	Human melanocortin
37	996.5	57.7	325	AAW49726	Sequence of a poly
38	994	57.6	323	AAW94427	Rhesus monkey mela
39	994	57.6	323	AAW60968	Murine melanocorti
40	994	57.6	323	AAE20595	Mus musculus melan
41	982.5	56.9	360	AAU95520	Human olfactory an
42	981.5	56.9	360	AAW19703	Melanocortin-3 rec
43	981.5	56.9	360	AAW79686	Melanocortin-3 rec
44	981.5	56.9	360	AAW33723	Human melanocortin
45	981.5	56.9	360	AAW92441	Human MC3 protein.

ALIGNMENTS

RESULT 1

AAU76428

ID AAU76428 standard; Protein; 332 AA.

XX

AC AAU76428;

XX

DT 08-MAY-2002 (first entry)

XX

DE Canine melanocortin 4 receptor (MC4R).

XX

KW Melanocortin 4 receptor; MC4R; G-protein coupled receptor; dog;

KW appetite; metabolic disorder; cachexia; anorexia;

KW weaning-induced inappetence; growth; diabetes; cancer; renal failure;

KW cardiac disease; endotoxaemia; fever; hepatic lipidosis; infection;

KW inflammation; post partum sow; dairy cow; livestock; poultry;

KW shipping stress; crowding stress; obesity; vaccine.

XX

OS Canidae.

XX

PN EPI167386-A1.

XX

PD 02-JAN-2002.

XX

PF 26-JUN-2001; 2001EP-0305509.

XX

PR 26-JUN-2000; 2000US-213909P.

XX

PA (PFIZ) PFIZER PROD INC.

XX

PI Hickman MA, Houseknecht KL, Robertson AS;

XX WPI; 2002-156598/21.

DR N-PSDB; ABK15578.

DR

XX Novel canine or feline melanocortin 4 receptor polypeptide for
PT screening modulator compounds useful for treating cachexia, anorexia,
PT diabetes and cancer
XX
XX
PS Claim 22; Fig 4; 73pp; English.
XX
XX The invention describes a substantially pure canine or feline
XX melanocortin 4 receptor (MC4R) polypeptide (I). The polypeptide can be
CC used in the treatment of appetite-related or metabolic disorders
CC including cachexia, anorexia or weaning-induced inappetence and growth
CC lag, diabetes, cancer, renal failure, cardiac disease, endotoxaemia,
CC fever, hepatic lipodosis, infection or inflammation, in a post partum
CC sow, dairy cow, companion animal, livestock animal, poultry animal,
CC animal suffering from shipping or crowding stress, lactating animal,
CC obese animal or a gravid animal. (I) is useful in the generation of
CC antibodies, as reagents in diagnostic assays, identification of other
CC cellular gene products involved in the regulation of appetite in animals,
CC as reagents in assays for screening for compounds that can be used in the
CC treatment of appetite disorders in animals. A ligand of MC4R is useful
CC for elaborating the biological function of MC4R gene product and for
CC ameliorating appetite disorders and metabolic disorders, in animals. This
CC is the amino acid sequence of the canine melanocortin 4 receptor (MC4R).
CC a G-protein coupled receptor described in the method of the invention.
XX
XX Sequence 332 AA:
XX
Query Match 100.0%; Score 1726; DB 23; Length 332;
Best Local Similarity 100.0%; Pred. No. 7.2e-180;
Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MNSTLQHGHTSLHFWNRSTYGOHGNATESLGKGYDPGGCYEOLFVSPEVFTLVISLL 60
Db 1 MNSTLQHGHTSLHFWNRSTYGOHGNATESLGKGYDPGGCYEOLFVSPEVFTLVISLL 60
QY 61 ENILVIVATAKNNLHSPMYFFICSLAVADMVLSVNSGSETIVITLLNSTDDAQSFYN 120
Db 61 ENILVIVATAKNNLHSPMYFFICSLAVADMVLSVNSGSETIVITLLNSTDDAQSFYN 120
QY 121 IDNVDSVICSSLLASICSLLSTAVDRYFTIFVALQYHNIMTVRRVGGIIISCIWAACVTS 180
Db 121 IDNVDSVICSSLLASICSLLSTAVDRYFTIFVALQYHNIMTVRRVGGIIISCIWAACVTS 180
QY 181 GILFIYSDSTAVIICLITMFTTMLALMASLVVHMFMLARLHKRIAVLPGTGTIRQGAN 240
Db 181 GILFIYSDSTAVIICLITMFTTMLALMASLVVHMFMLARLHKRIAVLPGTGTIRQGAN 240
QY 241 MKGATLTLLIGVFVVCWAPFLLHLIFYISCPQNPYCVCFMSHFNLYLLIMCNSIIDPL 300
Db 241 MKGATLTLLIGVFVVCWAPFLLHLIFYISCPQNPYCVCFMSHFNLYLLIMCNSIIDPL 300
QY 301 IYALRSQELRKTFFKEIICCYPLGGLCDLSSRY 332
Db 301 IYALRSQELRKTFFKEIICCYPLGGLCDLSSRY 332
RESULT 2
AAU76427
ID AAU76427 standard; Protein; 332 AA.
XX
AC AAU76427;
XX
XX 08-MAY-2002 (first entry)
DT
DE Feline melanocortin 4 receptor (MC4R).
XX
XX Melanocortin 4 receptor; MC4R; G-protein coupled; receptor; cat;
KW appetite; metabolic disorder; cachexia; anorexia;
KW weaning-induced inappetence; growth; diabetes; cancer; renal failure;
KW cardiac disease; endotoxaemia; fever; hepatic lipodosis; infection;
KW inflammation; post partum sow; dairy cow; livestock; poultry;
KW shipping stress; crowding stress; obesity; vaccine.
XX

OS Felidae.
XX
PN EP1167386-A1.
XX
PD 02-JAN-2002.
XX
XX 26-JUN-2001; 2001EP-0305509.
XX
XX 26-JUN-2000; 2000US-213909P.
XX
PA (PFIZ) PFIZER PROD INC.
XX
PI Hickman MA, Houseknecht KL, Robertson AS;
XX WPI: 2002-156598/21.
XX N-PSDB; ABK15577.
XX
XX Novel canine or feline melanocortin 4 receptor polypeptide for
PT screening modulator compounds useful for treating cachexia, anorexia,
PT diabetes and cancer
XX
XX Claim 3; Fig 3; 73pp; English.
XX
XX The invention describes a substantially pure canine or feline
CC melanocortin 4 receptor (MC4R) polypeptide (I). The polypeptide can be
CC used in the treatment of appetite-related or metabolic disorders
CC including cachexia, anorexia or weaning-induced inappetence and growth
CC lag, diabetes, cancer, renal failure, cardiac disease, endotoxaemia,
CC fever, hepatic lipodosis, infection or inflammation, in a post partum
CC sow, dairy cow, companion animal, livestock animal, poultry animal,
CC animal suffering from shipping or crowding stress, lactating animal,
CC obese animal or a gravid animal. (I) is useful in the generation of
CC antibodies, as reagents in diagnostic assays, identification of other
CC cellular gene products involved in the regulation of appetite in animals,
CC as reagents in assays for screening for compounds that can be used in the
CC treatment of appetite disorders in animals. A ligand of MC4R is useful
CC for elaborating the biological function of MC4R gene product and for
CC ameliorating appetite disorders and metabolic disorders, in animals. This
CC is the amino acid sequence of the feline melanocortin 4 receptor (MC4R).
CC a G-protein coupled receptor described in the method of the invention.
XX
XX Sequence 332 AA:
XX
Query Match 97.6%; Score 1685; DB 23; Length 332;
Best Local Similarity 97.6%; Pred. No. 2.2e-175;
Matches 324; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 MNSTLQHGHTSLHFWNRSTYGOHGNATESLGKGYDPGGCYEOLFVSPEVFTLVISLL 60
Db 1 MNSTLQHGHTSLHFWNRSTYGOHGNATESLGKGYDPGGCYEOLFVSPEVFTLVISLL 60
QY 61 ENILVIVATAKNNLHSPMYFFICSLAVADMVLSVNSGSETIVITLLNSTDDAQSFYN 120
Db 61 ENILVIVATAKNNLHSPMYFFICSLAVADMVLSVNSGSETIVITLLNSTDDAQSFYN 120
QY 121 IDNVDSVICSSLLASICSLLSTAVDRYFTIFVALQYHNIMTVRRVGGIIISCIWAACVTS 180
Db 121 IDNVDSVICSSLLASICSLLSTAVDRYFTIFVALQYHNIMTVRRVGGIIISCIWAACVTS 180
QY 181 GILFIYSDSTAVIICLITMFTTMLALMASLVVHMFMLARLHKRIAVLPGTGTIRQGAN 240
Db 181 GILFIYSDSTAVIICLITMFTTMLALMASLVVHMFMLARLHKRIAVLPGTGTIRQGAN 240
QY 241 MKGATLTLLIGVFVVCWAPFLLHLIFYISCPQNPYCVCFMSHFNLYLLIMCNSIIDPL 300
Db 241 MKGATLTLLIGVFVVCWAPFLLHLIFYISCPQNPYCVCFMSHFNLYLLIMCNSIIDPL 300
QY 301 IYALRSQELRKTFFKEIICCYPLGGLCDLSSRY 332
Db 301 IYALRSQELRKTFFKEIICCYPLGGLCDLSSRY 332
RESULT 3

AAW19704
ID AAW19704 standard; Protein; 332 AA.

XX
AC AAW19704;

XX
DT 19-AUG-1997 (first entry)

XX
DE Melanocortin-4 receptor.

XX
KW Melanocortin-3; MC3R; MC1R; MC2R; MC4R; MC5R; human; mouse; melanocyte;
KW pro-opiomelanocortin; adrenal cortical function; behaviour; learning;
KW memory; cardiovascular system; analgesia; thermoregulation; prolactin;
KW neurohumoral agent; biogenic amine.

XX
OS Homo sapiens.

XX
PN US5622860-A.

XX
PD 22-APR-1997.

XX
PF 17-FEB-1994; 94US-0200711.

XX
PR 17-FEB-1994; 94US-0200711.

XX
PA (UNMI) UNIV MICHIGAN.

XX
PI Gantz I, Yamada T;

XX
DR WPI; 1997-244394/22.

XX
DR N-PSDB; AAT68790.

XX
PT Nucleic acid molecules encoding melanocortin receptors - useful to
PT transfect mammalian cells lacking endogenous receptors to induce
PT their expression

XX
PS Claim 4; Column 43-46; 58pp; English.

XX
AAW19703-W19707 represent the human and mouse melanocortin (MC)
receptors. This sequence represents the MC4R, expressed primarily in
brain, but absent in the adrenal cortex, melanocytes and placenta. The
gene encoding this sequence is located at chromosome locus 18q21.3. MCs
are products of pro-opiomelanocortin post-translational processing, and
are known to have a broad array of physiological actions. MCs are known
to have effects on adrenal cortical functions and on melanocytes, as well
as affecting behaviour, learning, memory, control of the cardiovascular
system, analgesia, thermoregulation and the release of other neurohumoral
agents (such as prolactin and biogenic amines). The nucleic acids can be
used to transfect mammalian cells lacking endogenous MC receptors to
induce their expression. These sequences can also be used to screen and
identify drugs which specifically react with MCs on the surface of a
cell. The drugs can then be used for treating diseases which have MCs
implicated as one of their causes. Vectors containing these sequences can
also be used to treat the diseases.

XX
SQ Sequence 332 AA;

Query Match 94.9%; Score 1638.5; DB 18; Length 332;

Best Local Similarity 95.5%; Pred. No. 2.6e-170;

Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 1 MNSTLQHGHTSLHFWNRSTYQHGHNATSLGKGYPDGCGYEQLFVSPVFTLGVISLL 60

DB 2 VNST-HRCGMHTSLHFWNRSSYRLHNSASESLGKGYSDGCGYEQLFVSPVFTLGVISLL 60

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DB 61 ENILVIVAIAKNKNLHSPWYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120

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DB 121 IDNVDSVICSLLASCSLLSIAVDYFTTFYALQYHNIMTVRVGIIISCIWAACVTS 180

QY 181 GILFIYSDSTAVIICLTMTFTMLMASLYVHMFMLARLHKRIAVLPCTGTRQGAN 240

DB 181 GILFIYSDSTAVIICLTMTFTMLMASLYVHMFMLARLHKRIAVLPCTGTRQGAN 240

QY 241 MKGATLTLLIGVFWVWCHAPFLHLIFVYSCPNPCYCVCFKSHFNLYLLILMCNSTIDPL 300

DB 241 MKGATLTLLIGVFWVWCHAPFLHLIFVYSCPNPCYCVCFKSHFNLYLLILMCNSTIDPL 300

QY 301 IYALRSQELRKTFKEIICCYPLGGLCDLSSRY 332

DB 301 IYALRSQELRKTFKEIICCYPLGGLCDLSSRY 332

RESULT 4

AAW79687

ID AAW79687 standard; Protein; 332 AA.

XX
AC AAW79687;

XX
DT 17-DEC-1998 (first entry)

XX
DE Melanocortin-4 receptor.

XX
KW Human melanocortin-4 receptor; MC4; MC1; MC3; therapeutic; brain;
KW adrenal cortex; melanocyte; placenta.

XX
OS Homo sapiens.

XX
PN US5817787-A.

XX
PD 06-OCT-1998.

XX
PF 23-APR-1997; 97US-0842045.

XX
PR 17-FEB-1994; 94US-0200711.

XX
PR 27-JUN-1996; 96US-0672109.

XX
PR 23-APR-1997; 97US-0842045.

XX
PA (UNMI) UNIV MICHIGAN.

XX
PI Gantz I, Yamada T;

XX
DR WPI; 1998-556471/47.

XX
DR N-PSDB; AAV62352.

XX
PT DNA encoding melanocortin-5 receptor - useful in hybridisation
PT assays for melanocortin-5 receptor nucleic acids

XX
PS Disclosure; Column 43-46; 58pp; English.

XX
The present sequence represents the human melanocortin-4 (MC4) receptor,
the gene of which has been localised to chromosome 18q21.3. This
receptor is activated by both the amino and carboxyl terminal end amino
acids of melanocortins and has been found to be expressed primarily in
the brain and is absent from the adrenal cortex, melanocytes and
placenta. The DNA sequence that produces this polypeptide was identified
by using oligonucleotides constructed from previously identified
receptors MC1 and MC3, this was performed by using these oligonucleotides
to search genomic DNA for other members of the receptor family. These
genes and their products may be used to provide therapeutic vehicles for
the treatment of processes involving the function of melanocortin
receptors.

XX
SQ Sequence 332 AA;

Query Match 94.9%; Score 1638.5; DB 19; Length 332;

Best Local Similarity 95.5%; Pred. No. 2.6e-170;

Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 1 MNSTLQHGHTSLHFWNRSTYQHGHNATSLGKGYPDGCGYEQLFVSPVFTLGVISLL 60

DB 2 VNST-HRCGMHTSLHFWNRSSYRLHNSASESLGKGYSDGCGYEQLFVSPVFTLGVISLL 60

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Db 61 ENILVIVAIKAKNKLHSPMYFFICSLAVADMLVSVNGSETIIITLNSTDTDAQSFVN 120
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Db 121 IDNVDSVICSSLLASICSLLSTAVDRYFTIFVALQYHNIMTVRRVGIISCIWAACVS 180
Qy 181 GILFIYSDSTAVIICLITMFFTMLALMASLYVHMFMLARLHKRIKRIAVLPGTGAIROGAN 240
Db 181 GILFIYSDSSAVIICLITMFFTMLALMASLYVHMFMLARLHKRIKRIAVLPGTGAIROGAN 240
Qy 241 MKGAITLTILIGVFWVWAPFFLHLIFYISCPQNPYCVCPMSHFNLILIMCNSIIDPL 300
Db 241 MKGAITLTILIGVFWVWAPFFLHLIFYISCPQNPYCVCPMSHFNLILIMCNSIIDPL 300
Qy 301 IYALRSOELRKTEKEIICCCYPLGGLCDLSRY 332
Db 301 IYALRSOELRKTEKEIICCCYPLGGLCDLSRY 332

```

RESULT 5

AAW33724
ID AAW33724 standard; Protein; 332 AA.

AC AAW33724;

XX 30-APR-1998 (first entry)

DT Human melanocortin-4 (MC4) receptor.

DE Human melanocortin receptor; ligand; MC4; human.

XX Homo sapiens.

OS US5703220-A.

PN 30-DEC-1997.

PD 27-JUN-1996; 96US-0671525.

PF 17-FEB-1994; 94US-0200711.

PR 27-JUN-1996; 96US-0671525.

XX (UNMI) UNIV MICHIGAN.

PA Gantz I, Yamada T;

PI WPI; 1998-076484/07.

XX N-PSDB; AAV06400.

XX DNA encoding human melanocortin-4 receptor - and cells useful in

PT assay for MC4 receptor ligands

XX Claim 1; Columns 43-46; 59pp; English.

XX This is a human melanocortin receptor-4 (MC4). The MC4 receptor of this invention is activated by amino acids in the carboxyl and amino terminal portions of the heptapeptide sequence shared by all the melanocortin peptides. MC4 is expressed primarily in brain and is notably absent in the adrenal cortex, melanocytes and placenta. The MC4 receptor gene was localised to chromosome loci 18q21.3. The invention provides methods to identify ligands that bind to MC4 receptor.

XX Sequence 332 AA;

Query Match 94.9%; Score 1638.5; DB 19; Length 332;

Best Local Similarity 95.5%; Pred. No. 2.6e-170;

Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

Qy 1 MNSTLQHGMMHTSLHFWNRSTYGOHGNATESLGKYPDGGCYEQLFVSPFVTLGVISLL 60

Db 2 VNST-HRGMMHTSLHFWNRSTYLRHSNASESLGKYGDCGCEQLFVSPFVTLGVISLL 60

```

Qy 61 ENILVIVAIKAKNKLHSPMYFFICSLAVADMLVSVNGSETIIITLNSTDTDAQSFVN 120
Db 61 ENILVIVAIKAKNKLHSPMYFFICSLAVADMLVSVNGSETIIITLNSTDTDAQSFVN 120
Qy 121 IDNVDSVICSSLLASICSLLSTAVDRYFTIFVALQYHNIMTVRRVGIISCIWAACVS 180
Db 121 IDNVDSVICSSLLASICSLLSTAVDRYFTIFVALQYHNIMTVRRVGIISCIWAACVS 180
Qy 181 GILFIYSDSTAVIICLITMFFTMLALMASLYVHMFMLARLHKRIKRIAVLPGTGAIROGAN 240
Db 181 GILFIYSDSSAVIICLITMFFTMLALMASLYVHMFMLARLHKRIKRIAVLPGTGAIROGAN 240
Qy 241 MKGAITLTILIGVFWVWAPFFLHLIFYISCPQNPYCVCPMSHFNLILIMCNSIIDPL 300
Db 241 MKGAITLTILIGVFWVWAPFFLHLIFYISCPQNPYCVCPMSHFNLILIMCNSIIDPL 300
Qy 301 IYALRSOELRKTEKEIICCCYPLGGLCDLSRY 332
Db 301 IYALRSOELRKTEKEIICCCYPLGGLCDLSRY 332

```

RESULT 6

AAW92442
ID AAW92442 standard; Protein; 332 AA.

XX AAW92442;

DT 21-APR-1999 (first entry)

XX Human MC4 protein.

DE Melanocortin-4 receptor; MC1; MC2; MC3; MC4; MC5; detection; probe;

XX receptor binding; secondary signalling; tissue distribution.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Protein 1..332 /note= "No stop codon given"

XX US5869257-A.

PN 09-FEB-1999.

XX 23-APR-1997; 97US-0842238.

XX 17-FEB-1994; 94US-0200711.

PR 27-JUN-1996; 96US-0671525.

XX 23-APR-1997; 97US-0842238.

XX (UNMI) UNIV MICHIGAN.

PI Gantz I, Yamada T;

XX WPI; 1999-152760/13.

DR N-PSDB; AAX01964.

XX Probe for detecting melanocortin-4 receptor genes - that

PT specifically hybridises to defined DNA sequence

XX Example 1; Column 45-46; 60pp; English.

XX This sequence represents the human melanocortin-4 receptor, MC4. This protein is used in a method in which a nucleic acid probe useful for specifically detecting melanocortin-4 receptor genes is described.

CC This probe is used to isolate genes encoding melanocortin receptors.

CC to characterise melanocortin receptor binding and secondary signalling

CC and to determine tissue distribution of the melanocortin receptors.

XX Sequence 332 AA;

Query Match 94.9%; Score 1638.5; DB 20; Length 332;

Best Local Similarity 95.5%; Pred. No. 2.6e-170;

Example 11; Page 71; 120pp; English.

New methods are described by which membrane polypeptides can be labelled. The method comprises chemoselective chemical ligation of the membrane polypeptide which is incorporated in a lipid matrix, and a ligation label. Both contain an amino acid having an unprotected reactive group that together undergo chemoselective ligation to form a covalent bond. The method can be used to label folded polypeptides embedded in a lipid membrane, by treating the polypeptide with a reagent that cleaves specifically adjacent to an amino acid with an unprotected reactive group and then ligating the cleaved polypeptide with the ligation label. The ligation label can be a chromophore, thus ligand binding to membrane bound polypeptides can be detected by contacting a membrane bound polypeptide comprising a chromophore, with the ligand under investigation and screening for binding in an assay characterized by detecting fluorescence resonance energy transfer (FRET) between the chromophore and a second chromophore, the chromophores comprising a donor and acceptor pair of a resonance energy transfer system. The methods are used for lipid matrix-assisted chemical ligation and synthesis of membrane polypeptides. Labeled membrane polypeptides are used to detect ligand binding and the identification of receptor domains, e.g. for structure/activity studies. They can also be used in drug screening, selection or design, and for diagnosis. The methods are particularly used for fluorescent resonance energy transfer (FRET) analysis of previously inaccessible membrane polypeptides. The method allows site-specific incorporation of labels during polypeptide synthesis and analysis of previously inaccessible membrane proteins. A Melanocortin receptor MC4 which also comprises a Factor Xa cleavage site (AAV83182) can be cleaved with Factor Xa to give a C-terminal alpha-thioester modified MC4 receptor ligation label (AAV83183) and an MC4 receptor membrane polypeptide cleavage product (AAV83184). Chemical ligation of cleaved MC4 in alternative membrane patches or micelles to an MC4 ligation label produces this synthetic labeled MC4 product (AAV83185).

Sequence 332 AA;

Query Match 94.9%; Score 1638.5; DB 21; Length 332;
Best Local Similarity 95.5%; Pred. No. 2.6e-170;
Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 1 MNSTLQHGHTSIHFWRNSTYQHGHNATESLGKGYDGGCYEQLFVSPVEFVTLGVISLL 60
DB 2 VNST-HRGHTSLHLNRRSSYRLHNSASESLGKGYSDGGCYEQLFVSPVEFVTLGVISLL 60
QY 61 ENILVIVATAKKNLHSPMYFFICSLAVADMVLSVNSGSETIVITLLNSTDTDAQSFTVN 120
DB 61 ENILVIVATAKKNLHSPMYFFICSLAVADMVLSVNSGSETIVITLLNSTDTDAQSFTVN 120
QY 121 IDNVDSVTCSSLLASICSLLSIADVRYFTIFVALQYHNIMTVRRVGGIIISCIWAACVTS 180
DB 121 IDNVDSVTCSSLLASICSLLSIADVRYFTIFVALQYHNIMTVRRVGGIIISCIWAACVTS 180
QY 181 GILFIYSDSTAVIICLTIMFTMLMASLVHMFMLARLHKRIAVLPGTGTROGAN 240
DB 181 GILFIYSDSSAVIICLTIMFTMLMASLVHMFMLARLHKRIAVLPGTGTROGAN 240
QY 241 MKGAILTLTILGVVVCWAPFFLHLIFYISCPQNPVCVCFMSHFNLYLLIMCNSTIDPL 300
DB 241 MKGAILTLTILGVVVCWAPFFLHLIFYISCPQNPVCVCFMSHFNLYLLIMCNSTIDPL 300
QY 301 IVALRSQELRKTKEIICCYPLGGLCDLSSRY 332
DB 301 IVALRSQELRKTKEIICCYPLGGLCDLSSRY 332

RESULT 9

AAB68490
ID AAB68490 standard; Protein; 332 AA.
XX
AC AAB68490;
XX

DT 23-JUL-2001 (first entry)
XX Amino acid sequence of a human melanocortin-4 receptor (MC-R4).
DE Human: melanocortin-4 receptor; MC-R4; transgenic animal; body weight;
XX food intake; obesity; diabetes; anorexia; cachexia; cancer;
KW sexual dysfunction; pain; impaired memory; neuronal regeneration;
KW neuropathy; growth disorder; growth hormone;
KW insulin-like growth factor-1.
XX Homo sapiens.
XX WO200133956-A1.
PN 17-MAY-2001.
XX 13-NOV-2000; 2000WO-US31061.
PF 12-NOV-1999; 99US-0165074.
PR (MERI) MERCK & CO INC.
XX Van Der Ploeg LHT, Chen AS, Chen HY, Forrest MJ, MacIntyre DE;
PI Metzger JM, Palyha OC, Feighner SD, Hreniuk D;
XX N-PSDB; AAF85465.
DR WPI; 2001-343541/36.
XX New transgenic animal with non-functional gene for melanocortin-4
PT receptor, useful for identifying specific modulators, potentially used
PT for treating obesity or diabetes
XX Disclosure; Fig 2; 58pp; English.
PS The present sequence represents a human melanocortin-4 receptor (MC-R4).
XX The specification describes transgenic non-human animals whose somatic
CC and germ cells contain at least one non-functional gene for MC-4R
CC protein. The transgenic animals, or cells derived from them, are used
CC to screen for compounds that modulate MC-4R. These modulators are
CC potentially useful for regulating body weight and food intake and
CC treatment of associated diseases, obesity; diabetes; anorexia; cachexia;
CC cancer; sexual dysfunction; pain; impaired memory or neuronal
CC regeneration; neuropathy; growth disorders linked to growth hormone
CC and insulin-like growth factor-1. They can also be used to study MC-4R
CC expression and activity.
XX SQ Sequence 332 AA;
Query Match 94.9%; Score 1638.5; DB 22; Length 332;
Best Local Similarity 95.5%; Pred. No. 2.6e-170;
Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;
QY 1 MNSTLQHGHTSIHFWRNSTYQHGHNATESLGKGYDGGCYEQLFVSPVEFVTLGVISLL 60
DB 2 VNST-HRGHTSLHLNRRSSYRLHNSASESLGKGYSDGGCYEQLFVSPVEFVTLGVISLL 60
QY 61 ENILVIVATAKKNLHSPMYFFICSLAVADMVLSVNSGSETIVITLLNSTDTDAQSFTVN 120
DB 61 ENILVIVATAKKNLHSPMYFFICSLAVADMVLSVNSGSETIVITLLNSTDTDAQSFTVN 120
QY 121 IDNVDSVTCSSLLASICSLLSIADVRYFTIFVALQYHNIMTVRRVGGIIISCIWAACVTS 180
DB 121 IDNVDSVTCSSLLASICSLLSIADVRYFTIFVALQYHNIMTVRRVGGIIISCIWAACVTS 180
QY 181 GILFIYSDSTAVIICLTIMFTMLMASLVHMFMLARLHKRIAVLPGTGTROGAN 240
DB 181 GILFIYSDSSAVIICLTIMFTMLMASLVHMFMLARLHKRIAVLPGTGTROGAN 240
QY 241 MKGAILTLTILGVVVCWAPFFLHLIFYISCPQNPVCVCFMSHFNLYLLIMCNSTIDPL 300
DB 241 MKGAILTLTILGVVVCWAPFFLHLIFYISCPQNPVCVCFMSHFNLYLLIMCNSTIDPL 300
QY 301 IVALRSQELRKTKEIICCYPLGGLCDLSSRY 332

PI Sausker EA;
XX WPI; 2002-082744/11.
DR N-PSDB; AAD25896, AAD25897.
XX
PT Novel polymorphic variants of melanocortin 4-receptor gene useful in
PT studying expression and function of the protein, useful for screening
PT candidate drugs to treat diseases related to the protein activity e.g.
PT obesity
XX
PS Claim 27; Fig 3; 53pp; English.
XX
CC The invention relates to single nucleotide polymorphisms (SNP) in human
CC melanocortin 4-receptor (MC4R) gene. MC4R gene haplotypes are useful
CC for improving the efficiency and reliability of several steps in the
CC discovery and development of drugs for treating diseases associated
CC with MC4R activity, e.g. obesity. MC4R gene is useful in studying the
CC expression and function of MC4R and in expressing MC4R protein for
CC use in screening for candidate drugs to treat diseases related to
CC MC4R activity and in studying the effect of the variation on the
CC biological activity of MC4R as well as on the binding affinity of
CC candidate drugs targeting MC4R for the treatment of obesity. MC4R
CC antibody is useful in a variety of diagnostic and prognostic formats
CC and in therapeutic methods. Allele-specific oligonucleotide (ASO) is
CC useful as probes and primers, and for assaying a polymorphism in
CC MC4R gene. MC4R DNA is used in gene therapy. The present sequence is
CC human MC4R protein. MC4R gene is located on chromosome 18q22.
XX
SQ Sequence 332 AA;

Query Match 94.6%; Score 1632.5; DB 23; Length 332;
Best Local Similarity 95.2%; Pred. No. 1.2e-169;
Matches 316; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

QY 1 MNSTLQHGHTSLHFWNRSTYQHGHNATESLGKGYDPGCGYEQLFVSPFVTLGVISLL 60
DB :||||| ||||||| ||||| :| :||||| ||||||| ||||||| ||||||| |||||||
2 VNST-HRGHTSLHLWNRSYRLHNSASESLGKGYSDGCGYEQLFVSPFVTLGVISLL 60
QY 61 ENILVIAIAKKNLHSPMYFFICSLAVADMVSVNSGSETIVITLLNSTDTDAQSFTVN 120
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
61 ENILVIAIAKKNLHSPMYFFICSLAVADMVSVNSGSETIIITLLNSTDTDAQSFTVN 120
QY 121 IDNVDSVICSLLASICSLLSIAVDRTFTFYALQYHNIMTVRRVGIISCIWAACVTS 180
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
121 IDNVDSVICSLLASICSLLSIAVDRTFTFYALQYHNIMTVRRVGIISCIWAACVTS 180
QY 181 GILFIYSDSTAVIICLTMTFMTLALMASLVVHMFMLARLHKRIAVLPGTGTROGAN 240
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
181 GILFIYSDSTAVIICLTMTFMTLALMASLVVHMFMLARLHKRIAVLPGTGTROGAN 240
QY 241 MKGAILTLIGVFVVCWAPFLHLIFVISCPCQNPYCVCFMSHFNLYLILMCSNIIIDPL 300
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
241 MKGAILTLIGVFVVCWAPFLHLIFVISCPCQNPYCVCFMSHFNLYLILMCSNIIIDPL 300
QY 301 IYALRSQELRKFKEIICYPGGLCDLSRRY 332
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
301 IYALRSQELRKFKEIICYPGGLCDLSRRY 332

OS Homo sapiens.
OS Synthetic.
PN WO200022131-A2.
XX
PD 20-APR-2000.
PF 13-OCT-1999; 99WO-US24065.
XX
PR 13-OCT-1998; 98US-0170496.
PR 12-NOV-1998; 98US-0108029.
PR 20-NOV-1998; 98US-0109213.
PR 27-NOV-1998; 98US-0110060.
PR 16-FEB-1999; 99US-0120416.
PR 26-FEB-1999; 99US-0121852.
PR 12-MAR-1999; 99US-0123944.
PR 12-MAR-1999; 99US-0123945.
PR 12-MAR-1999; 99US-0123946.
PR 12-MAR-1999; 99US-0123948.
PR 12-MAR-1999; 99US-0123949.
PR 28-MAY-1999; 99US-0123951.
PR 28-MAY-1999; 99US-0136436.
PR 28-MAY-1999; 99US-0136437.
PR 28-MAY-1999; 99US-0136439.
PR 28-MAY-1999; 99US-0137127.
PR 28-MAY-1999; 99US-0137131.
PR 28-MAY-1999; 99US-0137567.
PR 30-JUN-1999; 99US-0141448.
PR 27-AUG-1999; 99US-0151114.
PR 03-SEP-1999; 99US-0152524.
PR 29-SEP-1999; 99US-0156633.
PR 29-SEP-1999; 99US-0156655.
PR 29-SEP-1999; 99US-0156634.
XX
XX (AREN-) ARENA PHARM INC.
PA Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;
PI Gore M, Lilaw CW, Lin I, Lowitz K, White C;
XX WPI: 2000-317986/27.
DR N-PSDB; AAA46119.
XX
PT Non-endogenous, human G protein-coupled receptors for screening
PT receptor, inverse or partial agonists useful as therapeutic agents
PS Example 2; Page 176-177; 187pp; English.
XX
CC The present invention describes transmembrane receptors, preferably
CC human G protein coupled receptors (GPCR), for which the endogenous
CC ligand is unknown (orphan GPCR receptors). More specifically the present
CC invention relates to non-endogenous, constitutively activated versions
CC of a human GPCR. These non-endogenous human GPCRs can be useful for
CC the direct identification of candidate compounds as receptors agonists,
CC inverse agonists or partial agonists for use as pharmaceutical agents.
CC AAA46017 to AAA46126 and AAA02825 to AAA02859 represent sequences used in
CC the exemplification of the present invention.
XX
SQ Sequence 332 AA;

Query Match 94.3%; Score 1627.5; DB 21; Length 332;
Best Local Similarity 94.9%; Pred. No. 4.2e-169;
Matches 315; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 MNSTLQHGHTSLHFWNRSTYQHGHNATESLGKGYDPGCGYEQLFVSPFVTLGVISLL 60
DB 2 VNST-HRGHTSLHLWNRSYRLHNSASESLGKGYSDGCGYEQLFVSPFVTLGVISLL 60
QY 61 ENILVIAIAKKNLHSPMYFFICSLAVADMVSVNSGSETIVITLLNSTDTDAQSFTVN 120
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
61 ENILVIAIAKKNLHSPMYFFICSLAVADMVSVNSGSETIIITLLNSTDTDAQSFTVN 120
QY 121 IDNVDSVICSLLASICSLLSIAVDRTFTFYALQYHNIMTVRRVGIISCIWAACVTS 180
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
121 IDNVDSVICSLLASICSLLSIAVDRTFTFYALQYHNIMTVRRVGIISCIWAACVTS 180

Db 121 IDNVDSVICSLLASICSLSIAVDRTYTFYALQYHNIMTVKRVGSGISCIWAACVTS 180
Qy 181 GILFIYSDSTAVIICLITMFTMLALMASLYVHMFMLARLHKRIAVLPCTGTGTAIRQAN 240
Db 181 GILFIYSDSTAVIICLITMFTMLALMASLYVHMFMLARLHKRIAVLPCTGTGTAIRQAN 240
Qy 241 MKGAITLILIGVFWVCWAPFLLHIFVYISCPQNPYCYCFMSHFNLYLILIMCNSIIDPL 300
Db 241 MKGAITLILIGVFWVCWAPFLLHIFVYISCPQNPYCYCFMSHFNLYLILIMCNSIIDPL 300
Qy 301 IYALRSQELRKTKEIICCYPLGLCLDLSRY 332
Db 301 IYALRSQELRKTKEIICCYPLGLCLDLSRY 332

RESULT 13

AA94301

ID AA94301 standard; Protein; 332 AA.

XX AC

AA94301;

XX DT

04-AUG-2000 (first entry)

XX DE

Rhesus monkey melanocortin-4 receptor protein.

XX KW

Rhesus monkey; rhodopsin; G-protein coupled receptor; anorectic;

XX KW

melanocyte stimulating hormone; melanocortin receptor; obesity.

XX OS

Macaca mulatta.

XX PN

WO200027863-A1.

XX PD

18-MAY-2000.

XX PF

05-NOV-1999; 99WO-US25767.

XX PR

09-NOV-1998; 98US-0107721.

XX PA

(MERI) MERCK & CO INC.

XX PI

MacNeill DJ, Weinberg DH, Van Der Ploeg LHT;

XX DR

WPI; 2000-376480/32.

XX DR

N-ESDB; AAA26972.

XX PT

Novel DNA encoding rhesus monkey melanocortin 4 receptor protein,

XX PT

recombinant vectors and host cells, useful in methods for identifying

XX PT

selective agonists and antagonists

XX PS

Claim 27; Page 35; 53pp; English.

XX CC

The present sequence is the rhesus monkey melanocortin-4

XX CC

receptor protein (MC-4R). Melanocortin receptors belong to the rhodopsin

XX CC

sub-family of G-protein coupled receptors. They bind and are

XX CC

activated by peptides such as alpha-, beta-, or gamma-melanocyte

XX CC

stimulating hormones derived from the pro-opiomelanocortin gene and they

XX CC

are believed to mediate a wide range of physiological functions.

XX CC

The rhesus MC-4R gene was isolated by PCR using a series of four

XX CC

oligonucleotides (AAA26973-A26976) based on the human MC-4R gene sequence

XX CC

and designed to incorporate a restriction enzyme site for cloning into

XX CC

the expression vector pCI-neo. The recombinant vector was transformed

XX CC

into DH5a cells in preparation for DNA sequencing. The MC-4R gene

XX CC

sequence (AAA26972) or a mutated form may be introduced into an

XX CC

expression vector for expression in host cells. The subcellular

XX CC

membrane fractions will comprise either wild-type or mutant forms of

XX CC

rhesus MC-4R at enhanced levels and can be used in assays to identify

XX CC

ligand binding, activators and modulators, agonists and antagonists of

XX CC

MC-4R. This will allow for selection of compounds that are active for

XX CC

the rhesus receptor in vitro and will allow the selection of novel

XX CC

drugs to treat obesity.

XX CC

Sequence 332 AA;

XX SQ

Query Match 94.1%; Score 1624.5; DB 21; Length 332;
Best Local Similarity 94.6%; Pred. No. 8.9e-169;
Matches 314; Conservative 7; Mismatches 10; Indels 1; Gaps 1;
Qy 1 MNSTLQHMHTSLHFWNRSTYQGRGNATGESLGKYPDGGCYEQLFVSPVFTLVGISLL 60
Db 2 VNST-HRGMHASLHLWNRSSHLNASESLGKYGSDGGCYEQLFVSPVFTLVGISLL 60
Qy 61 ENILVIVAIANKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAOSFTVN 120
Db 61 ENILVIVAIANKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDTQSFVN 120
Qy 121 IDNVDSVICSLLASICSLSIAVDRTYTFYALQYHNIMTVKRVGSGISCIWAACVTS 180
Db 121 IDNVDSVICSLLASICSLSIAVDRTYTFYALQYHNIMTVKRVGSGISCIWAACVTS 180
Qy 181 GILFIYSDSTAVIICLITMFTMLALMASLYVHMFMLARLHKRIAVLPCTGTGTAIRQAN 240
Db 181 GILFIYSDSTAVIICLITMFTMLALMASLYVHMFMLARLHKRIAVLPCTGTGTAIRQAN 240
Qy 241 MKGAITLILIGVFWVCWAPFLLHIFVYISCPQNPYCYCFMSHFNLYLILIMCNSIIDPL 300
Db 241 MKGAITLILIGVFWVCWAPFLLHIFVYISCPQNPYCYCFMSHFNLYLILIMCNSIIDPL 300
Qy 301 IYALRSQELRKTKEIICCYPLGLCLDLSRY 332
Db 301 IYALRSQELRKTKEIICCYPLGLCLDLSRY 332
RESULT 14
AA93182
ID AA93182 standard; protein; 332 AA.
XX AC
AA93182;
XX DT
24-JUL-2000 (first entry)
XX DE
Melanocortin receptor MC4 comprising Factor Xa cleavage site.
XX KW
Membrane polypeptide; lipid matrix; synthesis; ligation;
XX KW
chemoselective ligation; fluorescence resonance energy transfer;
XX KW
FRET; chromophore; ligand; receptor domain; drug screening;
XX KW
diagnosis; ion channel; melanocortin receptor; MC4.
XX OS
Synthetic.
XX OS
Homo sapiens.
XX PN
WO200012536-A2.
XX PD
09-MAR-2000.
XX PF
26-AUG-1999; 99WO-US19542.
XX PR
31-AUG-1998; 98US-0144964.
XX PR
05-MAR-1999; 99US-0263971.
XX PA
(GRYP-) GRYPHON SCI.
XX PI
Kochendoerfer GG, Hunter CL, Kent SBH, Botti P;
XX WPI; 2000-270792/23.
XX PT
Selectively labeled membrane peptides, useful e.g. for detecting ligand
XX PT
binding to receptors and in drug screening, are prepared, in lipid
XX PT
matrix, by reaction between amino acid residues
XX PS
Example 11; Page 68-69; 120pp; English.
XX CC
New methods are described by which membrane polypeptides can be
XX CC
labelled. The method comprises chemoselective chemical ligation of
XX CC
the membrane polypeptide which is incorporated in a lipid matrix,
XX CC
and a ligation label. Both contain an amino acid having an
XX CC
unprotected reactive group that together undergo chemoselective

Db 301 IYALRSQELRKTKEIICCYPLGGICDLSSRY 332

Search completed: June 4, 2003, 18:15:43
Job time : 52 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 14, 2003, 11:25:54 ; Search time 210 Seconds
(without alignments)

13687.622 Million cell updates/sec

Title: US-09-884-211A-2

Perfect score: 1985

Sequence: 1 ctaagaccgtggggaggcag.....gaataaaaaaaaaa 1985

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1029858 seqs, 72403093 residues

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1985	100.0	1985	9	US-09-884-211A-2
2	1166.6	58.8	1708	9	US-09-884-211A-1
3	968.6	48.8	1950	9	US-09-910-180-1
4	939	47.3	1671	9	US-10-288-160-15
5	426	21.5	978	9	US-10-288-160-17
6	424.8	21.4	1650	12	US-10-052-545-15
7	406.6	20.5	1675	10	US-09-903-395-1
8	387.4	19.5	1338	9	US-10-288-160-11
9	306.6	15.4	1270	12	US-10-052-545-1
10	303.4	15.3	1633	9	US-10-288-160-5
11	279	14.1	1260	9	US-10-288-160-3
12	279	14.1	1260	10	US-09-815-944-19
13	275.4	13.9	2012	9	US-10-151-431-3
14	273.8	13.8	2012	9	US-10-288-160-7
15	252.8	12.7	1100	12	US-10-015-948-1
16	246	12.4	1108	9	US-10-151-431-5
17	241.2	12.2	1108	9	US-10-288-160-9
18	138.8	7.0	306	12	US-10-052-545-7
19	124.4	6.3	312	12	US-10-052-545-9

20	116.6	5.9	372	12	US-10-052-545-11	Sequence 11, Appl
21	106.2	5.4	200	10	US-09-903-395-4	Sequence 4, Appl
22	97.6	4.9	200	12	US-10-015-948-4	Sequence 4, Appl
23	83.8	4.2	285	12	US-10-052-545-5	Sequence 5, Appl
24	71.6	3.6	1146	9	US-10-028-156-7	Sequence 7, Appl
25	71.6	3.6	1146	9	US-10-029-401-7	Sequence 7, Appl
26	71.6	3.6	1146	9	US-10-029-372-7	Sequence 7, Appl
27	70.2	3.5	1137	12	US-10-037-616-3	Sequence 3, Appl
28	64.2	3.2	1062	10	US-09-771-063-3	Sequence 3, Appl
29	62.6	3.2	1062	9	US-10-084-507B-19	Sequence 19, Appl
30	62.6	3.2	1062	10	US-09-771-063-1	Sequence 1, Appl
31	62.6	3.2	1062	12	US-10-037-616-5	Sequence 5, Appl
32	62.6	3.2	1170	9	US-10-084-507B-16	Sequence 16, Appl
33	62.2	3.1	1032	9	US-09-971-228-2	Sequence 2, Appl
34	62.2	3.1	1089	10	US-09-993-844-14	Sequence 14, Appl
35	62.2	3.1	1149	9	US-09-971-228-1	Sequence 1, Appl
36	62.2	3.1	1149	9	US-09-759-514-1	Sequence 1, Appl
37	62.2	3.1	1376	9	US-09-971-228-4	Sequence 4, Appl
38	62.2	3.1	2776	12	US-10-037-616-1	Sequence 1, Appl
39	62.2	3.1	4063	9	US-10-092-154-1091	Sequence 1091, Ap
40	62.2	3.1	4063	10	US-09-764-847-1091	Sequence 1091, Ap
41	61.8	3.1	200	12	US-10-015-948-3	Sequence 3, Appl
c 42	60	3.0	583	10	US-09-864-761-20772	Sequence 20772, A
c 43	60	3.0	1959	10	US-09-864-761-4012	Sequence 4012, Ap
c 44	59.8	3.0	364	9	US-10-084-507B-14	Sequence 14, Appl
45	59.8	3.0	388	9	US-09-796-692-3532	Sequence 3532, Ap

ALIGNMENTS

RESULT 1

US-09-884-211A-2
; Sequence 2, Application US/09884211A
; Publication No. US20030032791A1

; GENERAL INFORMATION:

; APPLICANT: Alan et. al.

; TITLE OF INVENTION: NOVEL MELANOCORTIN-4 RECEPTOR SEQUENCES AND
; SCREENING ASSAYS TO IDENTIFY COMPOUNDS USEFUL

; IN REGULATING ANIMAL APPETITE AND METABOLIC RATE

; FILE REFERENCE: PC10743A

; CURRENT APPLICATION NUMBER: US/09/884, 211A

; CURRENT FILING DATE: 2000-06-26

; PRIOR FILING DATE: 60/213,909

; PRIOR FILING DATE: 2000-06-26

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn ver. 2.1

; SEQ ID NO 2

; LENGTH: 1985

; TYPE: DNA

; ORGANISM: Canine MC4R Nucleotide Sequence

US-09-884-211A-2

Query Match 100.0%; Score 1985; DB 9; Length 1985;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1985; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTAAGACCGTGGGAGGAGCAGCTGATGGACATGTGCACGAGATTTCAGCTCCTCGTGGC 60
|||||
Db 1 CTAAGACCGTGGGAGGAGCAGCTGATGGACATGTGCACGAGATTTCAGCTCCTCGTGGC 60

Qy 61 TCGGCGCAACTCGGAGAANTACTTGCACAGACCTCCTCAATGCGCTAGACTAAAGTT 120
|||||
Db 61 TCGGCGCAACTCGGAGAANTACTTGCACAGACCTCCTCAATGCGCTAGACTAAAGTT 120

Qy 121 AAGTGGAGTGGAGGACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG 180
|||||
Db 121 AAGTGGAGTGGAGGACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG 180

Qy 181 AAAAAAGAAAGACAGACTCTTTGAAGTAAAGATGAGCATTTTCAAGAAATCGAAGATGTTA 240
|||||
Db 181 AAAAAAGAAAGACAGACTCTTTGAAGTAAAGATGAGCATTTTCAAGAAATCGAAGATGTTA 240

QY 241 CAGTGAAGGTGATCGGAGCTGTACCTGGGAAGACAGTAAGAGCTCCACTGCCAGCCTTTTG 300
DB 241 CAGTGAAGGTGATCGGAGCTGTACCTGGGAAGACAGTAAGAGCTCCACTGCCAGCCTTTTG 300
QY 301 GAGCAGGACAGGTACTCAACACCTGGCAGGCCAGCTGGATCCTCAGAACCTTTGGGAGC 360
DB 301 GAGCAGGACAGGTACTCAACACCTGGCAGGCCAGCTGGATCCTCAGAACCTTTGGGAGC 360
QY 361 CACGGAGAGGGGGAACATCAACCGGGGCTCCCTGGCTGAGAGGGCCGAATCAGTCCCGA 420
DB 361 CACGGAGAGGGGAGAACATCAACCGGGGCTCCCTGGCTGAGAGGGCCGAATCAGTCCCGA 420
QY 421 GGGGTCTGCATACACTTTGTCAGATGAATCTCCACCCTTCAGCAGCGGAATGCAACACTT 480
DB 421 GGGGTCTGCATACACTTTGTCAGATGAATCTCCACCCTTCAGCAGCGGAATGCAACACTT 480
QY 481 CTCCTCACCTTCGGAAACCGCAGCAGCTACGGGACAGCAGCGCAACCGCACTGAGTCCCTTG 540
DB 481 CTCCTCACCTTCGGAAACCGCAGCAGCTACGGGACAGCAGCGCAACCGCACTGAGTCCCTTG 540
QY 541 GCAAAGGCTTACCCGACGGGGATGCTACGAGCAACTCTTCCTCTCCCGGAGGTGTTTCG 600
DB 541 GCAAAGGCTTACCCGACGGGGATGCTACGAGCAACTCTTCCTCTCCCGGAGGTGTTTCG 600
QY 601 TGACTCTGGGGTCAATAGCTTGCCTGGAGAACATTTCTGGTGATCGTGGCAATAGCCAAGA 660
DB 601 TGACTCTGGGGTCAATAGCTTGCCTGGAGAACATTTCTGGTGATCGTGGCAATAGCCAAGA 660
QY 661 ACAAGAATCTGCACATCACCATGTACTTTTTCATCTGTAGCCTGGCTGGCCGATATGTC 720
DB 661 ACAAGAATCTGCACATCACCATGTACTTTTTCATCTGTAGCCTGGCTGGCCGATATGTC 720
QY 721 TGGTGAGGCTTTCCAAACGGGTGAGAGACATCGTCATCACCTGTTTGAACAGTACGGGATA 780
DB 721 TGGTGAGGCTTTCCAAACGGGTGAGAGACATCGTCATCACCTGTTTGAACAGTACGGGATA 780
QY 781 CGGACGGCAGAGTTTACGGTGAATATGTAAATGTCATTTGACCTGGTGATCTAGCT 840
DB 781 CGGACGGCAGAGTTTACGGTGAATATGTAAATGTCATTTGACCTGGTGATCTAGCT 840
QY 841 CCTTCTCGCCCTCGATTTGACGCTGCTCAATTTGACGAGTGGACAGGTACTTTACTATCT 900
DB 841 CCTTCTCGCCCTCGATTTGACGCTGCTCAATTTGACGAGTGGACAGGTACTTTACTATCT 900
QY 901 TTTATGCCCTCCAGTACCATAACATCATGACGGTGAGCGGTTGGGATCATCATCAGTT 960
DB 901 TTTATGCCCTCCAGTACCATAACATCATGACGGTGAGCGGTTGGGATCATCATCAGTT 960
QY 961 GCATCTGGCGGCTTGCAGGCTGTCAGGATCTTGTTCATCATTTACTCGGACACTGTC 1020
DB 961 GCATCTGGCGGCTTGCAGGCTGTCAGGATCTTGTTCATCATTTACTCGGACACTGTC 1020
QY 1021 CTGTATCATCTGCTCATCACCATGTTCTCACCATGCTGGCCCTCATGGCTTCTCTCT 1080
DB 1021 CTGTATCATCTGCTCATCACCATGTTCTCACCATGCTGGCCCTCATGGCTTCTCTCT 1080
QY 1081 AGCTCCACATGTTCTCATGGCCAGACTGCATCAAGAGATCCCGTCTCCCGGGCA 1140
DB 1081 AGCTCCACATGTTCTCATGGCCAGACTGCATCAAGAGATCCCGTCTCCCGGGCA 1140
QY 1141 CCGGCACCATCCGCAAGGGCCACATGAGGGTGCCATTTACCTTGACCATCATCTG 1200
DB 1141 CCGGCACCATCCGCAAGGGCCACATGAGGGTGCCATTTACCTTGACCATCATCTG 1200
QY 1201 GGGTCTTGTCTGCTGCGGGCTCCATCTTCTCCACTGTATATCTACATCTCTCTGTC 1260
DB 1201 GGGTCTTGTCTGCTGCGGGCTCCATCTTCTCCACTGTATATCTACATCTCTCTGTC 1260
QY 1261 CCCAGAATCCACTGCTGTGCTTCTCATGTCCTTAACTTTGACCTCATCTTGTGATCA 1320
DB 1261 CCCAGAATCCACTGCTGTGCTTCTCATGTCCTTAACTTTGACCTCATCTTGTGATCA 1320
QY 1321 TGTGTAACCTCATCATCGACCTCTCATTTATGCACTCCGGAGCCAGAGCTGAGGAAAA 1380

DB 1321 TGTGTAACCTCATCATCGACCTCTCATTTATGCACTCCGGAGCCAAAGAGCTGAGGAAAA 1380
QY 1381 CCTTCAAAGAGATCATCTGTTCTCTATCCCTCGGTGGCCCTTGTGACTTGTCTAGCAGAT 1440
DB 1381 CCTTCAAAGAGATCATCTGTTCTCTATCCCTCGGTGGCCCTTGTGACTTGTCTAGCAGAT 1440
QY 1441 ACTAGCTGGGGACAGAGGAAGTACTAAAAACATGACCAAGAGACTTCTTCATCCTCACAC 1500
DB 1441 ACTAGCTGGGGACAGAGGAAGTACTAAAAACATGACCAAGAGACTTCTTCATCCTCACAC 1500
QY 1501 AACATGAACCTGCTGTTGGACACAGCTGCTTCTTCTAGTATATAAGSCAGAGTGTGAAAT 1560
DB 1501 AACATGAACCTGCTGTTGGACACAGCTGCTTCTTCTAGTATATAAGSCAGAGTGTGAAAT 1560
QY 1561 ATCTGCTGCACAAATTCACATTTATCATGTTTATGATGTGAAAAAATAATGCCAGGCTC 1620
DB 1561 ATCTGCTGCACAAATTCACATTTATGATGTTTATGATGTGAAAAAATAATGCCAGGCTC 1620
QY 1621 TGTACATTTGCTAATGCTGCTACTTTTGGGCTGTGCAATTTTAAATCCATTTTCGAGCTG 1680
DB 1621 TGTACATTTGCTAATGCTGCTACTTTTGGGCTGTGCAATTTTAAATCCATTTTCGAGCTG 1680
QY 1681 TAGACACTTTGAAATTTCTAGAAAAAGAAAAAGCTTCCATTTAAAGCATATCATGTTTCT 1740
DB 1681 TAGACACTTTGAAATTTCTAGAAAAAGAAAAAGCTTCCATTTAAAGCATATCATGTTTCT 1740
QY 1741 TGTATTTACAGAGGATTTGGCACTTTGCTTGTCTTTAGGAAACATAGAAATCATAGATCA 1800
DB 1741 TGTATTTACAGAGGATTTGGCACTTTGCTTGTCTTTAGGAAACATAGAAATCATAGATCA 1800
QY 1801 TTAACATATGACCTGTAAAGTAACTTCTTATATTTATATATACATATACATGAAATGTCAG 1860
DB 1801 TTAACATATGACCTGTAAAGTAACTTCTTATATTTATATATACATATACATGAAATGTCAG 1860
QY 1861 ATTTGAATGTAGCATGGGGGTGGATATTTGAACATATAGATCTTGGTCATTAAAAACAATC 1920
DB 1861 ATTTGAATGTAGCATGGGGGTGGATATTTGAACATATAGATCTTGGTCATTAAAAACAATC 1920
QY 1921 AACTCAAAATTTTAACTAAATAAAATGTTTCAATTCCTCTGTCAGAAAAATAAAAAAAA 1980
DB 1921 AACTCAAAATTTTAACTAAATAAAATGTTTCAATTCCTCTGTCAGAAAAATAAAAAAAA 1980
QY 1981 AAAAA 1985
DB 1981 AAAAA 1985

RESULT 2

US-09-884-211a-1
; Sequence 1, Application US/09884211a
; Publication No. US20030032791A1
; GENERAL INFORMATION:
; APPLICANT: Alan et. al.
; TITLE OF INVENTION: NOVEL MELANOCORTIN-4 RECEPTOR SEQUENCES AND
; TITLE OF INVENTION: SCREENING ASSAYS TO IDENTIFY COMPOUNDS USEFUL
; TITLE OF INVENTION: IN REGULATING ANIMAL APPETITE AND METABOLIC RATE
; FILE REFERENCE: PC10743A
; CURRENT APPLICATION NUMBER: US/09/884,211a
; CURRENT FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 60/213,909
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1708
; TYPE: DNA
; ORGANISM: Feline MCR Nucleotide Sequence
US-09-884-211a-1

Query Match 58.8%; Score 1166.6; DB 9; Length 1708;
Best Local Similarity 83.5%; Pred. No. 1.8e-297;
Matches 1418; Conservative 0; Mismatches 224; Indels 57; Gaps 6;

QY	14	GAGCGAGCTGATCGGAACATGTCGACGAGATTACGTCCTGCTGGTGGCTCGGCGGCAACTC	73
Db	64	GAGCGAGCTGGTGTGAACATGTCGAACACGCGATTTCAGCTCCCACTGGCGACAGCAGCCACTA	123
QY	74	GGAAATTAATCTGCAACAGACACCTCTACTGTAATGCCCTAGACTAAAGTTAAGTGGGAGTGGA	133
Db	124	GGAAATTAATTTGAAAGACCTGACTGATGCTCAGGCTAAAGTTAGGTGGGAAGGGA	183
QY	134	GGACAAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAG	193
Db	184	GGACA-----GAAAAGCAAAAG	201
QY	194	CAGACTCTTTGAACCTAAGATGAGCATTTTCAGAAATCGAAGATGTTACAGTGAAGGTGAT	253
Db	202	CAGACTCTTTCAACTCAGAAATGAGTATTTTCAGAAAGCCTAAGATTTTACAAATGAAGGTGAT	261
QY	254	CGGAGCTGTACCTTGGGAAGACAGTAAGAGCTGCCACTGCCAGCCCTTTTGGACGACGGGACAG	313
Db	262	CAGAGCCGTTCCTGGGAGACAGTAAAACTCCATTTCCAGCC--TGGGAGCAGCTGACAT	319
QY	314	GTACTCAACACCTGGCAGGCCAGCTGGATCCTCAGAACTTTGGACGCAAGGAGAGGGGG	373
Db	320	TTTACTC-ACAACAGGCAATGCCAATTTTCAGCCTCAGAACTTTTCGGCGCAGACAAAGGCGTGG	378
QY	374	AGAACATCAGCGGGGTCCTTGCTGGAGAGGCCGGAATCAGTCCCGAGGGGGTCTGCATA	433
Db	379	AGAAAACACTGAGGTACCTTGACCCGAGAGATCGAATCAATTTCCGAGGGGATCTGAATC	438
QY	434	CACCTGTTCAGAGATGAACCTCCACCCCTTCAGCAGCGAATCACACTTCTCTCCACTTCTG	493
Db	439	CAC-TGGTGCAGATGAACTCCACTCATCACCATGGAATGCACACTTCTCTCCACTTCTG	497
QY	494	GAACCGAGCACCTACGGACAGCAGCGCAACGCCACTGAGTCCTCTGGCAAAAGGCTACCC	553
Db	498	GAACCGCAGCACCTACGGACCGCAGCAATGCCAGTGCCTGAGTCCCTTTGGAAAAGGCTACTC	557
QY	554	CGAGGGGGATGCTACGAGCAACTCTTCGCTCTCCCGGAGGTGTTTCGTGACTCTGGGGT	613
Db	558	TGATGAGGGGTGTATGAGCAACTTTTGTGTCCTCCCTGAGGTGTTGTGACTCTGGGTGT	617
QY	614	CATAAGCTTGTGGAGAACAATCTTGCTGATCGTGGCAATAGCCAAAGAACTGTGCA	673
Db	618	CATCAGCTTGTGGAGATATCTTGGTGATTTGGCAATAGCCAAAGAACTGTGCA	677
QY	674	CTCACCAGTACTTTTTCACTGTAGCTGGCTGTGGCGGATATGCTGGTGAAGCTTTC	733
Db	678	TTCCGCCATGATCTTTTTTCATCTGCAAGCTGGCTGTGGCTGATATGTTGGTGAAGCTGTC	737
QY	734	CAACGGGTGAGACACCATCGTATCATCCCTGTTTGAACAGTACGGAATACGCAAGCGAGAG	793
Db	738	AAACGATCCGAACCAATGTCATACCCCTATTAAACAGTACAGATACGCAAGCGGAGAG	797
QY	794	TTTCACGGTGAATTTGATAATGTCATTTGACTCGGTGATCTGTAGTCTCCTTGCTCGCCTC	853
Db	798	TTTTCACGGTGAATTTGATAATGTCATTTGACTCGGTGATCTGTAGTCTCCTTGCTTCGATC	857
QY	854	GATTTGAGCCTGCTCTCAATTCGAGTGGACAGGTACTTTTACTATCTTTTATGCCCTTCA	913
Db	858	GATTTGAGCCTGCTCTCAATTCGAGTGGACAGGTACTTTTACTATCTTTTATGCTCTCCA	917
QY	914	GTACCAATACATCATGACGGTGAAGCGGGTTGGATCATCATCAGTTGATCTGGGCGGC	973
Db	918	GTACCAATACATCATGACGGTGAAGCGGGTTGGATCATCATTAAGTTGTATCTGGGCAAGC	977
QY	974	TTGCACGGTGTACAGGACTCTTGTTCATCATTTTACTCGGACAGTACTGCTGTCAATCATCTG	1033
Db	978	TTGCACGGTGTTCGGGCGTTTGTGTTCATCATCTACTCAGACAGCAGTGTCTCATCATCTG	1037
QY	1034	CCTCATCACCATGTTCTTACCAATGCTGGCCCTCATGGCTTCTCTCTACGTCACATGTT	1093
Db	1038	CCTCATCACCATGTTCTTACCAATGCTGGCTCTCATGGCTCTCTCTATGTCACATGTT	1097

Qy	1094	CCTCATGGCCAGACTGCACATCAAGAGAAATCGCGCTCTCCGGGACACGGCACCACATCCG	1155
Db	1098	CCTCATGGCCAGACTGCACATTAAGAGAAATTCGTCTCTCCGGGCACTGGCACCACATCCG	1157
Qy	1154	CCAAAGGGCCAAACATGAAGGGTGCATTACCTTTGACCATACTCATTTGGGGTCTTTGCTCGT	1213
Db	1158	CCAAAGGGCCAAACATGAAGGGTGCATTACCTTGACCATACTGATTGGGGTCTTTGTTGT	1217
Qy	1214	CTGCTGGGCTCCAAATCTTCTTCACACTTGATATTCTACATCTCTTTGCTCCCGAAGATCCATA	1273
Db	1218	CTGCTGGGCCCCCTTCTTCTCCACTTTAATATTCTACATCTCTTTGCTCCCGAAGATCCCTTA	1277
Qy	1274	CTGTGTCTGCTTCATGTCTCACTTTAACTTTGTACCTTCATTTCTGATCATGTGTAACCTCCAT	1333
Db	1278	CTGTGTCTGCTTCATGTCTCACTTTAACTTGTATCTCATACTGATCATGTGTAATTCAT	1337
Qy	1334	CATCGACCCCTCTCATTTTATGCATCCGGAGCCCAAGAGCTGAGGAAAACCTTCAAAGAGAT	1393
Db	1338	CATCGACCCCTCTAATTTATGCATCCGGAGCCCAAGAACTAAGGAAAACCTTCAAAGAGAT	1397
Qy	1394	CATCTGTTGCTATCCCTCTGGTGGCCCTTTGTGACTTTGTCTTAGCAGATACTAGCTGGGGAC	1453
Db	1398	CATCTGTTGCTATCCCTCTAGCGGCCCTCTGTGATTTGTCTAGCAGATACTAACTGTGTCAG	1457
Qy	1454	AGAGGAAGTACTAAAAACATGCACACGACGACTTCTTCATCCTCACACAAACATGAACGTGTG	1513
Db	1458	A-----TAGAAACGTGCATAGAGACTTCTTCATCTTTACAGAACCCGNAACATTG	1507
Qy	1514	TGCTTGGACAACAGCTGCTCTTCAGTATTAAGCAGGAGTTGAGAAATATCTGTTGCACAA	1573
Db	1508	TGCTTTGATGACCCCTTTCTCCTCTGTGTGAAGGCATGGTGTGAGACTATCTGTTGTATAA	1567
Qy	1574	ATTCACACTTTATGATGTTTGTAGTGTGAAAAAAAATATGCCAGGCTCTGTACATTGCTAA	1633
Db	1568	ATTTAAGTTTCATGACTTTTTTTTTTGGAAATGAAAACAATGCCACGCTCTGTACATTCTCAA	1627
Qy	1634	TGTCATGCTACTTTTTGGGCTGTGCATTTGTTTAATCCCAT-TTTCGACGCTGTAGACACTTTGA	1692
Db	1628	TGTCCTGCTACTTTTTTGCTGTACAATGTTTAATCCCATATTATAGTTGTAGGCACATATGA	1687
Qy	1593	ATTTCTAGAAAAAGAAAAA	1711
Db	1688	ATGTTATAAAAAATAAAAAA	1706

RESULT, T 3

```

RESOLUT 3
US-09-910-180-1
: Sequence 1, Application US/09910180
: Publication No. US20030082678A1
: GENERAL INFORMATION:
: APPLICANT: Hs lung, Hansen
: APPLICANT: Smith, Dennis
: APPLICANT: Zhang, Xing-yue
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
: FILE REFERENCE: P-17621
: CURRENT APPLICATION NUMBER: US/09/
: CURRENT FILING DATE: 2002-04-11
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: Patentin version 3.1
: SEQ ID NO 1
: LENGTH: 1950
: TYPE: DNA
: ORGANISM: Bovine
US-09-910-180-1

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[illegible]

QY 284 CCACTGCCAGCCTTTTGGAGCAGGGGACAGAGGTACTCAACACCTGGCAGGCGCAGCTGGATC 343
Db 128 TCTTTTCCAGC--TCCGGAGCATGGGACATTTATTC-ACAGGAGGCCTCCACTCTCCGC 184
QY 344 CTCAGAACTTTGGGAGC---CACGGAGAGGGGAGAACATCACCAGGGCTCCCTGGCTG 399
Db 185 CGCCTAACCTTTTGGTGGGCAAGTCAAGACTGGAGAAAGGTGCTGAGGCTGCCAGATCC 244
QY 400 GAGAGCGGAATCAGTCCCGAGGGGTCTGCATACACTTTGTCAGAGATGAATCCACOC 459
Db 245 AGGAGGTCAGTCAGTCAGGAGGGGACCTGAATCCAAA-----ATGAACTCTACCC 295
QY 460 TTCAGACAGGAATGCACACTTCTCCCACTTCTGGAACCGCAGCAGCTACGAGCAGCAG 519
Db 296 AGCCCCCTGGGATGCACACTCTCTCCACTCTGGAACCGCAGCAGCGCCACGGAATGCCCA 355
QY 520 GAAAGCCCACTCAGTCCCTTGGCAAGGCTACCCGAGGGGATCTACGAGCACTCT 579
Db 356 CCATGTCTAGTCCCTGGCAAGGCTACTCGGACGGGGGTGCTATGAGCAGCTCT 415
QY 580 TCGTCTCCCGGAGGTGTTCGTGACTCTGGGGTTCATAGCTTTGCTGGAGAACATTTCTGG 639
Db 416 TTGTCTCTCCCGAGGTGTTCGTGACTCTGGGGTTCATGACTTTGTTGGAGATATTCGG 475
QY 640 TGATCGTGCAATAGCCAAAGAACAGAAATCTGCACCTCACCCATGTACTTTTCATCTGTA 699
Db 476 TGATCGTGCCCATAGCAAGAACAGAAATCTGCACCTCACCCATGTACTTTTCATCTGCA 535
QY 700 GCCTGGCTGTGCCGATATGCTGGTGAGGGTTTCAACGGGTCAGAGACCATCGTCATCA 759
Db 536 GCCTGGCTGTGGCTGACATGTGTGGAGGGTTTCAACGGGTCGGAACCATTTGTCATCA 595
QY 760 CCCTGTTGAACAGTACGGATACGGACCGCGCAGAGTTTTCACGGTGAATATTTGAATGTCA 819
Db 596 CCCTGCTGAACAGCAGGACACGGACCGCGCAGAGCTTCACGGTGGATATTTGACATGTCA 655
QY 820 TTGACTCGGTATCTGTAGCTCCTTCTGCTGCCCTCGATTTGACGCTGCTCTCAATTGCGAG 879
Db 656 TTGACTCGGTGATCTGTAGCTCCTTCTGCTGCCCTCGATTTGACGCTGCTCTGCTGCGCGG 715
QY 880 TGGACAGGTACTTTTACTATCTTTTATGCGCTCCAGTACCATAACATCATGACGGTGAGGC 939
Db 716 TGGACAGGTACTTTTACTATCTTTTATGCGCTCCAGTACCATAACATCATGACGGTGAGGC 775
QY 940 GGGTTGGGATCATCATAGTTTCATCTGGCGGGCTTGCACGGTGTGACGSCATCTTTGTTC 999
Db 776 GGGTGGCATCACCATCAGCGCCATCTGGCGAGCCTGCGAGGCTGTCGGGCGCTTTGTTC 835
QY 1000 TCATTACTCGCAGAGTACTGCTGTCTCATCTGCTGCTCATCACCATGTTCTTCACCATGC 1059
Db 836 TCATTACTCGACAGCAGTGTCTTATCATCTGCTCATCACCGCTTCTTCACCATGC 895
QY 1060 TGGCCCTCATGCTTCTCTACGTCCACATGTTCTCATGGCCAGACTGACATCAAGA 1119
Db 896 TGGCTCTCATGGCTCTCTATGTCCACATGTTCTCATGGCCAGACTGACATCAAGA 955
QY 1120 GAATCGCGTCTCTCCGGCACCAGCATCCGCCAAGGGGCCAACATGAAGGGTGCCA 1179
Db 956 GGATCGCGTCTCTCCAGGTAGCGGCACCATCCGCCAGGGCCCAACATGAAGGGGGCA 1015
QY 1180 TTACCTTGACCAATCATTTGGGGTCTTCGGGTCTGCTGGGCTCCATTCCTTCCTCCACT 1239
Db 1016 TTACCTTGACCAATCATTTGGGGTCTTCGGGTCTGCTGGGCTCCATTCCTTCCTCCACT 1075
QY 1240 TGATATTTACATCTCTTCCCGCAAGATTCATCTGCTGTGCTTCACTGCTCACTTTA 1299
Db 1076 TGATATTTACATCTCTTCCCGCAAGATTCATCTGCTGTGCTTCACTGCTCACTTTA 1135
QY 1300 ACTTGTACCTATCTGTGTAATCTCATCATCGACCTCTCATTTATGACACTCC 1359
Db 1136 ACCTGTACCTCATCTCATCTGTCGAATTCATCATGACCTCTGATTTATGCGCTGC 1195
QY 1360 GGAGCCAAAGAGCTGAGGAAAACCTTCAAAGAGATCATCTGTTGCTATCCTCTGGGTGCC 1419

RESULT 4

US-10-288-160-15

; Sequence 15, Application US/10288160

; Publication No. US20030105024A1

; GENERAL INFORMATION:

; APPLICANT: Cone, Roger D

; Fan, Wei

; Boston, Bruce A

; Kesterton, Robert A

; Lu, Dongsu

; Chen, Wenbiao

; TITLE OF INVENTION: Methods and Reagents for Discovering and

; Using Mammalian Melanocortin Receptor Agonists and Antag

; To Modulate Feeding Behavior in Animals

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff

; STREET: 300 South Wacker Drive

; CITY: Chicago

; STATE: IL

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/288,160

; FILING DATE: 05-NO. US20030105024A1-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/706,281

APPLICANT: Cone, Roger D
Fan, Wei
Boston, Bruce A
Kesterton, Robert A
Lu, Dongsi
Chen, Wenbiao

TITLE OF INVENTION: Methods and Reagents for Discovering and
Using Mammalian Melanocortin Receptor Agonists and Antagonists
To Modulate Feeding Behavior in Animals

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/288,160
FILING DATE: 05-No. US20030105024A1-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/706,281
FILING DATE: 04-SEP-1996

ATTORNEY/AGENT INFORMATION:
NAME: NO. US20030105024A1nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 96,886

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002

INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 978 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..975
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-288-160-17

Query Match 21.5%; Score 426; DB 9; Length 978;
Best Local Similarity 68.5%; Pred. No. 5,1e-102;
Matches 604; Conservative 0; Mismatches 275; Indels 3; Gaps 1;

QY 566 CTACGAGCAACTCTTCGCTCCCGGAGGTGTTCTGACTCTCGGGGTCAATAGCTTGT 625
DB 96 CTGTGAAGAATGGGCAATTCGCGTGGAGGTCTCTGACCCCTGGGTCTCGTCAGCCTCT 155

QY 626 GGAGACATCTCTGGTGTGCTGGCAATACCCAGACAGATCTGCACCTACCCATGTA 585
DB 156 AGAGAACATCTCTGGTGTGCTGGGCAATAGTAAGAAACAAACCTGCATACCCATGTA 215

QY 686 CTTTTCATCTCTAGCTGGCTGTGCGCCGATATGCTGTGAGCGTTTCCACGGGTGCGA 745
DB 216 CTTCTTTGGGCAGCTTAGCGGTGGCCGACATGCTGTGAGCATGTCCATGCTCGGGA 275

QY 746 GACCATCGTATACCCCTGTTGAACAGTACCGATACGG---ACGCGCAGAGTTTCCACGGT 802
DB 276 GACTGTCAACATATCTTGTCTAAATAAACAACCTGGTGTGATAGCCGACACCTTTTGTGG 335

QY 803 GAATATGATATGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 862
DB 336 ACACATCGACAAACGTTTCGAGTCCATGATCTGTCATCTCTGTGTGGTGGCCTCGATGTGCG 395

RESULT 6

US-10-052-545-15
; Sequence 15, Application US/10052545
; Patent No. US20020142392A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Melanocyte stimulating hormone receptor
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/052,545
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/387,805
; FILING DATE: 21-FEB-95
; APPLICATION NUMBER: PCT/DK93/00273
; FILING DATE: 20-AUG-93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 1046/92

FILING DATE: 21-AUG-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 1118/92
FILING DATE: 10-SEP-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0528/93
FILING DATE: 05-MAY-93
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1102.0160000
TELEPHONE: (202)371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1650 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (cDNA)
FEATURE:
NAME/KEY: CDS
LOCATION: 616..1590
US-10-052-545-15

Query Match 21.4%; Score 424.8; DB 12; Length 1650;
Best Local Similarity 69.2%; Pred. No. 1.5e-101; Indels 3; Gaps 1;
Matches 595; Conservative 0; Mismatches 262;

QY	590	GGAGGTGTTGCTGACCTGGGGTGCATAGCTTCTGGGAGAACATCTTGCTGATCGTGGC	649
DB	735	GGAGGTGTTTCTCACTCTGGGTGCATCAGCCCTTGGGAGAACATCTTGCTGATCGTGGC	794
QY	650	AATAGCCAGAGAACAAATCTGCATCACCATGACTTCTTTTCTGATCGTGGCTGT	709
DB	795	CATAGTGAAGAACAAAACCTGCATCCTCCCATGTACTTCTTCTGTCAGCTGGCAGT	854
QY	710	GGCGGATATGCTGGTGGGCTTCCAAAGGGTCCAGAGACCATCGTCATCACCCTGTGAA	769
DB	855	GGCGGACATGCTGGTGAGCATGTCAGTGCCTGGGAGACCATCACCATCTACCTCAAA	914
QY	770	CAGTACGGA---TACGGAGCGCGAGAGTTTACGGTGAATATTGATAATGCTATGACTC	826
DB	915	CAACAAGCACCTAGTGATAGACAGACGCTTTGTGGCGCCACATGACAATGTGTTGACTC	974
QY	827	GGTATCTGTAGTCTTCTGCTGCCCTGCAATTCGACGCTGCTCTCAATTCGATGGACAG	886
DB	975	CATGATCTGCATTTCCGTGGTGGCATCCATGTGCAGCTTACTGGCCATTTGCACTGGATAG	1034
QY	887	GTACTTTACTATCTTTTATGCCCTCCAGTACCATAACATCATCAGCGTGAGCGGGTTGG	946
DB	1035	GTACGTCACCATCTTCTACGCCCTGGCTACCAACACATCATACCGCGAGGCGCTCAGG	1094
QY	947	GATCATCATAGTTGATCTGGCGGCTTGCAGGGTGTACGGGATCTTGTTCATCATTTA	1006
DB	1095	GGCCATCATCGCGCGCATCTGGGCTTCTGCACGGGCTGGGCATGTTCTTCATCTCGTA	1154
QY	1007	CTCGGACAGTACTGCTGATCATCTGCTCATCAGCATGTTCTTCAACATGTCGCCCT	1066
DB	1155	CTCAAGTCCACCTACGATCTATCTGTGCTCATCTCTCCATCTTCTGGCTATGTTCTCT	1214
QY	1067	CATGGCTTCTCTACGTCACATGTTCTCATGGCCAGACTGCATCATCAAGAGATCGC	1126
DB	1215	CCTGGTGTCTCTGATACATCAATGTTCTTCTTGGCGGAGCTCAGCTCAAGCGGATCGC	1274
QY	1127	CGTCTCCCGGGCAGCGCACCATCCGCAAGGGGCGCAACATGAAGGGTGGCCATTACCTT	1186
DB	1275	GCTCTCGCGGGGCGAGCTCTGCGCGGAGAGACCATGAGGCGCGGCTACCGT	1334
QY	1187	GACCATCATGTTGGGCTCTGCTGCTGCTGGGCTCCATGTTCTTCCATCTGATATT	1246
DB	1335	CACCATGCTGCTGGGGTGTGTTACCGTGTGCTGGGCGCGGTTCTTCTTCTCATCTCACTT	1394

QY	1247	CTACATCTCTTGTCCCGAGAAATCCACTACTGTTGTGCTTCATGTCTCACTTTAACTTGA	1306
DB	1395	AATGCTTTCTTGTCCCTCAGAACCTTACTCTCTCGGTTCTGCTCCTCACTATATGTA	1454
QY	1307	CCTCATCTCTGATCATGTGTAACCTCAATCATCGACCCCTCTCATTTATGACATCGGAGCCA	1366
DB	1455	CCTCATACTCATCATGTGTAATCCGTTGATGAGACCCCTCTCATATATGCTTCCGAGCCA	1514
QY	1367	AGAGCTGAGGAAAACCTTCAAGAGATCATCTGTTGCTATCTCTCTGGTGGCCCTTTTGA	1426
DB	1515	AGAGATGCGGAGAACCTTTAAGGAGATTATTTGCTGCCGTTTTCAGATCGCCTGAG	1574
QY	1427	CTTGTCTAGCAGATACTAGC	1446
DB	1575	CTTCCAGAGAGGATTAAC	1594

RESULT 7

US-09-903-395-1
Sequence 1, Application US/09903395
Patent No. US20020068324A1
GENERAL INFORMATION:
APPLICANT: Allen, Keith D.
TITLE OF INVENTION: TRANSGENIC MICE CONTAINING
FILE REFERENCE: R-653
CURRENT APPLICATION NUMBER: US/09/903,395
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/218,074
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/243,958
PRIOR FILING DATE: 2000-10-26
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1675
TYPE: DNA
ORGANISM: Mus musculus
US-09-903-395-1

Query Match 20.5%; Score 406.6; DB 10; Length 1675;
Best Local Similarity 67.7%; Pred. No. 9.9e-97;
Matches 603; Conservative 0; Mismatches 279; Indels 9; Gaps 2;

QY	523	ACGCCACTGAGTCCCTTGGCAAGGCTACCCCGACGGGGATGCTACGACGAACTCTTCG	582
DB	168	ACCTCGACGCCCTCTCTGCCAGCAACCGGAGCGGAGTGGGTCTTGTGACGAGGCTCTTCA	227
QY	583	TCCTCCCGGAGGTGCTGCTGACTCTGGGGTCTAAGCTTCTGGGAGAACTTCTGGTGA	642
DB	228	TCAGCGGAGGCTTCTCTGGCTCTGGGCACTGCTGATGGAAGAACTCTGCTGGA	287
QY	643	TCGTGGCAATPAGCAAGAACAAATCTGCACCTCACCCATGATCTTTTTCATCTGTAGCC	702
DB	288	TCCTGGCTGTGGTCAGGAATGGCAACCTGCACTTCCCATGTACTTCTCTGTCGACGC	347
QY	703	TGCTGTGGCGGATATGCTGGTGAGCGTTTCCAAACGGGTCAGAGACCATGTCATCACCC	762
DB	348	TGGCTCGACGCGACATGCTGTGAGCCTGTCCAACCTCCCTGGAGACCATCATGATCCCG	407
QY	763	TGTTGAACAG---TAGGATACGACGCGCAGAGTTTTCACGGTGAATATTGATAATCTCA	819
DB	408	TGATCAACAGCGACTCCCTGACCTTGGAGGACCAAGTTTATCCAGCACATGATATATCT	467
QY	820	TTGACTCGGTGATCTGTAGTCTCTTGTCTGCCCTCGAATTTGACGCTCTCTCAATTGAG	879
DB	468	TCGACTATGATTTGATCTCTCCCTGCTGGGCTCCATCTGCAACCTCTTGGCCATTGCCA	527
QY	880	TGACAGGATCTTACTATCTTTTATGCTCCCTCCAGTACCATAACATCATGACGCTGAGGC	939
DB	528	TCGACAGGTACGTCACCATCTTCTATGCCCTTGGTACCACAGCATCATGACAGTTAGGA	587

QY 940 GGGTTGGGATCATCATAGTTGTCATCTGGGGGGCTTGGCAGCGGTGTGACGGCATCTTGTTC 999
Db 588 AAGCCCTACCTTGTACCTGGGTCATCTGGTCTGGCGCATCTGCGCGGTGATGTTC 647
QY 1000 TCATTTACTCGGACAGTACTGCTGTGCATCATCTGCTCATCACCAGTCTTCTCACCATGC 1059
Db 648 TCATCTACTCGGAGAGAGATGGTCATCGTGTGTCTCATCACCAGTCTTCTCGGCATGG 707
QY 1060 TGGCCCTCATGCTTCTCTACGTCCACATGTTCTCTCATGCGGAGCTGACATCAAGA 1119
Db 708 TGCTCTCATGGGACCCCTATATCCACATGTTCTCTTGGCCAGGCTCCAGTCCAGC 767
QY 1120 GAATCGCGCTCTCC-----CGGGCACCGGCACCATCCGCCAAGGGCCCAACATGAAG 1173
Db 768 GCATCGCAGTGTGCGCCCTGTGCGGTGGTGGCCACAGCAGCAGTCTCTGCATGAAG 827
QY 1174 GTGCCATTACCTTGACCATCTCATTTGGGGTCTTCTGCTGTGCGGCTCATCTCTCC 1233
Db 828 GGGTGTCCACCATCTATCTGCTGGGTGTTTTCATCTTCTGCTGGCGCTTCTTCTCC 887
QY 1234 TCCACTTGATATCTACATCTCTTGTGCCAGAACTTCTGCTGTGCTTCATGCTCTC 1293
Db 888 TCCACTGTGCTCATCATCATACCTGCCCCACCAATCCCTACTGATCTGCTACAGCGGCC 947
QY 1294 ACTTTAACTTGATCTCATCTGATCATGTGTAATCCATCATGACCCCTCTCATTTATG 1353
Db 948 ATTTCAACACCTACTGTTCTCATCATGTGCAACTCGTATCGACCCCTCATCTACG 1007
QY 1354 CACTCCGAGGACGAGCTGAGGAAACCTTCAAGAGATCATCTGTTGCT 1404
Db 1008 CTTTCCGAGGCTGAGCTGAGGACACGTTTCAAGGAGATCTCTGCGGCT 1058

RESULT 8

US-10-288-160-11
; Sequence 11, Application US/10288160
; Publication No. US20030105024A1
; GENERAL INFORMATION:
; APPLICANT: Cone, Roger D
; Pan, Wei
; Boston, Bruce A
; Resterton, Robert A
; Lu, Dongsi
; Chen, Wenbiao
; TITLE OF INVENTION: Methods and Reagents for Discovering and
; Using Mammalian Melanocortin Receptor Agonists and Antagonists
; To Modulate Feeding Behavior in Animals
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/288,160
; FILING DATE: 05-No. US20030105024A1-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/706,281
; FILING DATE: 04-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20030105024A1nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 96,886
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001

; TELEFAX: 312-913-0002
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1338 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..297
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 298..1269
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1270..1338
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-288-160-11
Query Match 19.5%; Score 387.4; DB 9; Length 1338;
Best Local Similarity 66.3%; Pred. No. 1e-91;
Matches 591; Conservative 0; Mismatches 291; Indels 9; Gaps 2;
QY 523 ACGCACGTAGTCCCTTGGCAAGGCTACCCCGACGGGGGATGCTACGAGCAACTCTTTCG 582
Db 356 ACCCTGACGCCCCCTCTGCCAGCAACCGAGTGGGATGCTGCCAGGAGGTTTCA 415
QY 583 TCTCCCCGAGGTGTTCTGTAAGCTCTGGGGGTGATAAGCTTCTGGAGAACATCTGTFGA 642
Db 416 TCAAGCCAGAGGTCTTCTGCGCATCGTCAGTCTGATGAAAAACATCTCTGTGA 475
QY 643 TCGTGGCANATAGCCCAAGACAAGATCTGCACTCACCATCTACTTTTCTCTGTAGCC 702
Db 476 TCTTGGCTGTGTGAGGAACGGCAACCTGCACTCCCCCATGTACTTCTTCTGTGAGCC 535
QY 703 TGGCTGTGGCGGATATGCTGTGAGCGTTTCCAAACGGGTGAGACCACTCGTCATCACC 762
Db 536 TGCTGACGCGACCTGCTGTGAGCGTGTCCAACTCCCTGGAGACCATCATGATCGGG 595
QY 763 TGTGAAACAG--TACGGATACGACGCGAGAGTTTCACGGTGAATATTGATATGCA 819
Db 596 TTATCAACAGAGACTCCCTGACCTTGGAGGACCAATTCATCCAGCAGCATGGAACAATCT 655
QY 820 TTGACTCGGTGATCTGTAGTCTTGTGCTCGCTCGATTTGGAGCTGCTCTCAATTGAG 879
Db 656 TCGACTCTATGATCTGCACTCTCCCTGGTGGGCTCCATCTGCAACCTCTGCGCATCGCGG 715
QY 880 TGGACAGGTACTTTTACTATCTTTTATGCCCTTCCAGTACCATACATCATGACGTTAGGC 939
Db 716 TGGACAGGTAGTCAACCATCTTCTATGCCCTCCGTACCACAGCATCATGACGTTAGGA 775
QY 940 GGGTTGGGATCATCATGTTGCAATCTGGGGGGCTTGCACCGGTGTGAGGCAATCTGTTTCA 999
Db 776 AAGCCCTCTCTTGTATGCTGGCCATCTGGGTCTGCTGTGGCATCTGCGCGCTGATGTTCA 835
QY 1000 TCATTTACTCGGACAGTACTGCTGTATCATCTGCTCATCTGCTCATCACCATGTTCTTACCATGC 1059
Db 836 TCGTCTACTCGGAGAGCAAGATGTCATCTGCTGCTCATCACCATGTTCTTCCGCAATGG 895
QY 1060 TGGCCCTCATGGCTTCTCTTACCTCCACATGTTCTCATGCGGAGCTGCGACATCAAGA 1119
Db 896 TGCTCTCATGGGACCCCTGTACATCCACATGTTCTTTCGCCAGGCTGACGCTCCAGC 955
QY 1120 GAATCGCGGCTCTCCCGGGCACCGGC-----ACCATCCGCCAAGGGGCCAACATGAAG 1173
Db 956 GCATCGGGGCACTGCCACCTGCTGACGGGCTAGCGCGGAGCAGCAGCACTCTGTCATGAAG 1015
QY 1174 GTGCCATTACTTGACCATCTCATTTGGGGTCTTCTGCTGCTGCTGCTGCTGCTTCTTCC 1233
Db 1016 GGGCGGTCACCATCACCATCTGCTGGGGGTTTTCATCTTCTGCTGGCGCTTCTTCTCC 1075

Qy 1234 TCCACTGATATCTACATCTCTGTGCCAGAAATCCATCATCTGTGTGCTTCTCATGTCTC 1293
Db 1076 TCCACCTGGTCTCTACATCATCTACCTGCCCAACCAACCTCTGCTGTCTACAGCGCG 1135
Qy 1294 ACTTTAACTTGTACCTCACTCTGATCATGTGTAACTTCACTCCATCATCGACCCCTCTCATTTATG 1353
Db 1136 ACTTCAACACTACCTGGTCTCTCATCATGTGCAACTCTGTGTCATCGACCCCTCATCTACG 1195
Qy 1354 CACTCCGAGCCAGAGCTGAGGAAACCTTCAAGAGATCATCTGTGTCT 1404
Db 1196 CCTCCGACCTGGAGCTCGAACAACCTTCAAGGAGATCTCTGCGGTT 1246

RESULT 9

US-10-052-545-1
; Sequence 1, Application US/10052545
; Patent No. US20020142392A1
; GENERAL INFORMATION:
; APPLICANT: Human Melanocyte stimulating hormone receptor
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/052,545
; FILING DATE:

CLASSIFICATION:

; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/387,805
; FILING DATE: 21-FEB-95
; APPLICATION NUMBER: PCT/DK93/00273
; FILING DATE: 20-AUG-93
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: DK 1046/92
; FILING DATE: 21-AUG-92
; APPLICATION NUMBER: DK 1118/92
; FILING DATE: 10-SEP-92
; APPLICATION NUMBER: DK 0528/93
; FILING DATE: 05-MAY-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbalà, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 1102.0160000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1270 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (cDNA)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 169..1122

US-10-052-545-1

Query Match 15.4%; Score 306.6; DB 12; Length 1270;
Best Local Similarity 61.3%; Pred. No. 2.1e-70;
Matches 530; Conservative 0; Mismatches 329; Indels 6; Gaps 2;

Qy 546 GGCTACCCGACGGGGATGCTACGAGCAACTCTTCGTCTCCCGAGGTTGTTCTGTGACT 605
Db 250 GCCAACCCAGACAGAGCCCGGTGCTGGAGGTGTCATCTCTGACGGGCTTCTCTCAGC 309
Qy 606 CTGGGGTCTAAGACTTTCCTGGAGAACATCTGTGTGATCGTGGCAATAGCAAGAACAAAG 665
Db 310 CTGGGGTGTGTAGCTTGGTGGAGAACGCGTGTGTGGCCACCATCTCGCCCAAGACCGG 369
Qy 666 AATCTGACATCACCACATGTAATTTTCATCTGTAGCTGCTGTGGCCGATATCTGTGTG 725
Db 370 AACCTGACATCACCACATGTAATTTTCATCTGTGCTGTGGCCGATATCTGTGTG 429
Qy 726 AGCGTTTTCACACGGGTGAGAGACCATGCTATCATCCCTGTTGAA---CAGTACGATACG 782
Db 430 AGCGGAGCAACGTTGCTGGAGACGGCGTCTCTCTGCTGGAGCGGTTGCTGCTGCTG 489
Qy 783 GACGCGCAGAGTTTCACGCTGAATATTTGATTAATGATTAATGATTAATGATTAATGATTA 842
Db 490 GCGCGGCTGCGGTGCTGTCAGACAGTGGACAATGTCATTTGACGTGATCACCTGACGTCC 549
Qy 843 TTGCTCGCTCGATTTTCAGCCTGCTCTCAATTCAGTGGACAGTACTTTTACTATCTTT 902
Db 550 ATGCTGTCCAGCTCTCTCTCTGGGCGCCATCCCGTGGACCCGTCATCTCCATCTCCTTC 609
Qy 903 TATGCCCTCCAGTACCATATAACATCATGACGCTGAGCGGGTTGGGATCATCATCAGTTGC 962
Db 610 TACGCACTGCGCTACCAACATCATGACCTGTCACCTGCGCGGGCGGCGGCGTTCGCGCC 669
Qy 963 ATCTGGCGGGTTCACGCTGTGACGATCTCTCAATTCAGTGGACAGTACTTTTACTGCT 1022
Db 670 ATCTGGTGGCCAGTGTGCTCTTTCAGCAGCTCTCTTCATCGCTACTACGACAGTGGCC 729
Qy 1023 GTCATCATCTGCCATCACCATGTTCTTACCATGCTGGCCCTCATGGCTTCTCTCTAC 1082
Db 730 GTCTGTGCTGCTGCTGCTGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 789
Qy 1083 GTCCACATGTTCTCATGCGGACAGTGCATCATCAAGAAATCGCC---GTCTCCCGGCG 1139
Db 790 GTCCACATGTTGCGCGCGGCTGCGACAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGG 849
Qy 1140 ACCGGCACCATTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1199
Db 850 CAGCGCGCGGTCCACAGGCGTTCGCGGCTTAAAGGCGCTGTCACCCCTCACCATCTGCTG 909
Qy 1200 GGGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1259
Db 910 GGCATTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 969
Qy 1260 CCCAGAAATCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1319
Db 970 CCCAGACCCCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1029
Qy 1320 ATGTGTAATCCATCATCGACCCCTCTCATTTATGATCGACTCCGGAGCCAGAGCTGAGGAA 1379
Db 1030 ATCTGCAATGCCATCATCGACCCCTCTCATCTACGCTTCCACAGCCAGAGGCTCGCGAGG 1089
Qy 1380 ACCTTCAAGAGATCATCTGTTGCT 1404
Db 1090 ACGCTCAAGAGGTTGCTGACATGCT 1114

RESULT 10

US-10-288-160-5
; Sequence 5, Application US/10288160
; Publication No. US20030105024A1
; GENERAL INFORMATION:
; APPLICANT: Cone, Roger D
; Fan, Wei
; Boston, Bruce A
; Kesterton, Robert A
; Lu, Dongsi
; Chen, Wenbiao


```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/706,281
; FILING DATE: 04-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20030105024Alnan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 96,886
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..14
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..959
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 960..1260
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-288-160-3

Query Match 14.1%; Score 279; DB 9; Length 1260;
Best Local Similarity 59.3%; Pred. No. 4.1e-63;
Matches 512; Conservative 0; Mismatches 345; Indels 6; Gaps 2;

QY 548 CTACCCGACGGGGATGCTACAGCAACTCTTCGTCCTCCCGAGGTGTTCGTGACTCT 607
Db 92 CAACCAAGTCAGAGCCCTTGGTGCCTATGTGTCCATCCAGATGGCCCTCTTCCTCAGCCT 151
QY 608 GGGGGTCATAAGCTTGTCTGGAGAACATTCCTGGTGATCGTGGCAATAGCCAAAGAA 667
Db 152 AGGCTGGTGAGTCTGGTGAGAAATGTCTGGTGTGATAGCAATACCAAAACCCGAA 211
QY 668 TCTGCACTACCCATGACTTTTTCATCTGTAGCTGGCTGTGSCCATATGCTGGTGAG 727
Db 212 CTTGCACTGCCCATGATTTACTTCACTGTCTGGCCCTGTCTGACCTGATGTTAG 271
QY 728 CGTTTCCAAAGGGTCAGAGACCATCGTCATCACCTGTTGAA---CAGTACGGATACGGA 784
Db 272 TGTACGATCGTGTGGAGACTACTATCATCTGCTGTGGAGGTGGGCACTCCCTGGTGGC 331
QY 785 CGCGCAGAGTTTCACGGTGAATATGTGATATGTCATGCTGGTGATCTGTAGCTCCTT 844
Db 332 CAGAGTGGCTTGGTCAGACGCTGGACAACCTCAATTGACGTGCTCATCTGTGGCTCCAT 391
QY 845 GCTCGCCTCGATTTGGCAGCTGCTTCAATTCAGTGGACAGGTGACTTTTACTATCTTTA 904
Db 392 GGTGTCCAGTCTCTGCTTCTCGGCATCATTTGATAGACCGGTACATCTCCATCTCTA 451
QY 905 TGGCTTCCAGTACCATACATCATAGCGGTGAGCGGGTGGGATCATCATAGTGCAT 964
Db 452 TGGCTGCGTATACAGCATCTGACGCTGCCAGAGCACGACGGGCTGCTGGGGCAT 511
QY 965 CTGGGGGCTTGCAGGCTGTGAGCATCTGTTTCATCATTTACTCGGACAGTACTGCTGT 1024
Db 512 CTGGATGGTCAGCATCGTCTCCAGCACCCCTTTTATACCTACTACAAAGCACACAGCCGT 571
QY 1025 CATCATCTGCTCATCACCATGTTCTTCAACATGCTGGCCCTCATGGCTTCTCTACGT 1084
Db 572 TCTGCTCTGCTGCTACATCTTCTTAGCCATGCTGGCACTCATGGCGATTTCTGTATGC 631
QY 1085 CCACATGTTCTCATGGCCAGACTGCACATCAAGAGAATCGCC---GTCTCCCGGGCAC 1141
Db 632 CCACATGTTTCACGAGAGCGGTGCCAGCAGCTCCAGGGCATTTGCCAGCTCCACAAAAGCG 691

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Db 332 CAGAGTGGCTTTGGTGACGAGCTGGACACCTCATTTGACGCTCTCATCTGTGGCTCCAT 391
QY 845 GCTCGCTCGATTGTCAGCGCTGCTCTCAATTTCAGTGGACAGGTACTTTTACTATCTTTTA 904
Db 392 GGTGTCCAGTCTCTGCTTCTCGGGCATCATGTATAGACCGGTATCATCTCCATCTCTTA 451
QY 905 TGCCCTCCAGTACCATAAACATGACGGTGGAGCGGTTGGGATCATCATCATAGTTCAT 964
Db 452 TGGCTGCGGTTATCACAGCATCTGACGCTGCCAGCAGCAGCGGCTGTCTGGGCAT 511
QY 965 CTGGGCGGCTTGACCGGTGTCAGGATCTGTTTCATCATTTACTCGGACAGTACTGCTGT 1024
Db 512 CTGGATGGTACAGCATGCTTCCAGCACCTCTTTTATCACCTACTACAAGCACACAGCGGT 571
QY 1025 CATCATCTGCCTCATCACCATGTTCTTCCACATGCTGGCCTCATGCTTCTCTACGT 1084
Db 572 TCTGCTCTGCTGCTGCTCTTCTTCTAGCATGCTGGCACTCATGGCATTCTGTATGC 631
QY 1085 CCACATGTTCCATGCGCAGACTGCACATCAAGAGAAATCGCC--GTCTCCCGGGCAC 1141
Db 632 CCACATGTTTACAGAGAGCTGGCAGCACGTCCAGGGCATTGCCAGCTCCACAAAAGCG 691
QY 1142 CGGCACCATCCGCCAAGGGCCACATGAAGGTGCCATTACTTGACCATCTCATTTGG 1201
Db 692 GCGGTCCATCCGCGCAAGGCTTGTGCTCAAGGGTGTGCCACCTTACTATCTTCTTGG 751
QY 1202 GGTCTTCTGCTGCTGCTGGCTCCATTCTTCTCCACTTGATTTACATCTTCTTGTCC 1261
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QY 1322 GTGTAACCTCATCATGACCCCTCTCATTTATGCACCTCCGGAGCCAGACCTGAGGAAAC 1381
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QY 1382 CTTCAAGAGATCATCTGTTGCT 1404
Db 932 ACTCAAGAGGTGCTGCTGTCT 954
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RESULT 13

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US-10-151-431-3
; Sequence 3, Application US/10151431
; Publication No. US20030044973A1
; GENERAL INFORMATION:
; APPLICANT: Cone, Roger D
; Mountjoy, Kathleen G
; TITLE OF INVENTION: Mammalian Adrenocorticotrophic Hormone
; Receptors and Uses
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Allegrretti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/151,431
; FILING DATE: 20-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,298
; FILING DATE: <Unknown>
```

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; APPLICATION NUMBER: US 07/866,560
; FILING DATE: 10-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20030044973Alban, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1200
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2012 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 694..1587
; OTHER INFORMATION: /product= "Human
; adrenocorticotrophic hormone receptor"
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..693
; NAME/KEY: 3'UTR
; LOCATION: 1588..2012
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-151-431-3
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Query Match 13.9%; Score 275.4; DB 9; Length 2012;
Best Local Similarity 60.8%; Pred. No. 5.1e-62;
Matches 497; Conservative 0; Mismatches 296; Indels 24; Gaps 2;

QY 590 GGAGGTGTTCTGAGTCTGTGGGGTCTAATAGCTTGTGGAGAACATTTCTGGTGTGCTGGC 649
Db 777 GGAGATATTTTTCACAAATTTCCATTTGTGGAGTTTGGAGAAATCTGATCGTCTGCTGGC 836
QY 650 AATAGCAAGAACAAGAAATCTGCACCTACCCCATGTACTTTTTCATCTGTAGCCTGGCTGT 709
Db 837 TGTGTTCAAGAATAAGAAATCTCCAGGCACCCATGTACTTTTTCATCTGTAGCTTGCCAT 896
QY 710 GGCCGATATGCTGGTGAGGCTTTCCAAACGGGTGAGAGACATCGTCAATCACCCTGTGAA 769
Db 897 ATCTGATATGCTGGGCAGCCTATATAAGATCTTGGAAATAATCTCTCATCATATTGAGAA 956
QY 770 CAGTACGGATACGGACGGC---AGAGTTTCAGGGTGAATATATGTCAATTTGACTC 826
Db 957 CATGGGCTATCTCAAGCCACGTGGCAGTTTGAACCCACAGCGGATGACATCATCGACTC 1016
QY 827 GGTGATCTGTAGTCTCTGCTGCGCTCGATTTGACGCTGCTCTCAATTCAGCTGACAG 886
Db 1017 CCGTTTGTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1076
QY 887 GTACTTTACTATCTTTTATGCGCCTCCAGTACCATCAATCATCATGACGGTGGAGCGGTGG 946
Db 1077 CTACATCACCATCTTCCACGCACTGGGTACACAGACCTGTCGACCATCGCGGCACTGT 1136
QY 947 GATCATCATCATGTGATCTGGGCGGCTTGCAGGGTGTGACGGTCTTGTTCATCATTTA 1006
Db 1137 GGTGGTGTCTAGGTCATCTGGACGTTCTGACGGGACTGGCATCACCATGGTGTATCTT 1196
QY 1007 CTCGGACAGTACTGCTGTCTCATCTGCTCATCACCATGTTCTTCCACATGCTGCGCT 1066
Db 1197 CTCCTCATGATGCGCCACAGTACCTTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTT 1256
QY 1067 CATGGCTTCTCTAGCTCCACATGTTCTCTCATGCGCAGACTGCACATCAAGAGAAATCGC 1126
Db 1257 CATCTGTGCTCTATGTGCACATGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1316
QY 1127 CGTCTCTCCGGGCAACCGGCAACCATCCGCAAGGGGCAACATGAGGGGTGCCATTTACCTT 1186
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Db 1317 CACCTCCCCAGA-----GCCAACAATGAAGGGGCCATCACACT 1355
Qy 1187 GACCATACCTATTGGGGTCTTCGGTCTGGCTCCCATCTTCTCCACTTGATATT 1246
Db 1356 GACCATCTGCTGGGGTCTTCATCTCTGCTGGGCCCTTTGCTTCATGCTCTCTT 1415
Qy 1247 CTACATCTCTGTCCCGAAGATCAATCAATCAATCAATCAATCAATCAATCAAT 1306
Db 1416 GATGACATCTTGCCTCAAGTAACTCCCTACTGGCTGCTGCTGCTGCTGCTGCT 1475
Qy 1307 CCTCATCTGATCATCTGCTCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1366
Db 1476 CGGATGTTGATCAATGCAATGCGCTCAATGACCCCTTCATATGCTTCCCGAGGCC 1535
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RESULT 14

US-10-288-160-7
; Sequence 7, Application US/10288160
; Publication No. US20030105024A1

GENERAL INFORMATION:

APPLICANT: Cone, Roger D
Fan, Wei
Boston, Bruce A
Kesterton, Robert A
Lu, Dongxi
Chen, Wenbiao

TITLE OF INVENTION: Methods and Reagents for Discovering and
Using Mammalian Melanocortin Receptor Agonists and Antagonists
To Modulate Feeding Behavior in Animals

NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:

ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/288,160
FILING DATE: 05-No. US20030105024A1-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/706,281
FILING DATE: 04-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: No. US20030105024Alnan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 96,886
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 2012 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA

FEATURE:

NAME/KEY: 5'UTR
LOCATION: 1..693
FEATURE:

NAME/KEY: CDS

; LOCATION: 694..1587
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1588..2012
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-288-160-7

Query Match 13.8%; Score 273.8; DB 9; Length 2012;
Best Local Similarity 60.7%; Pred No. 1.4e-61;
Matches 496; Conservative 0; Mismatches 297; Indels 24; Gaps 2;

Qy 590 GGAGGTGTTCTGACTCTGGGGGTCAATAAGCTTGTCTGGAGAACATCTCTGGTGAATCGCTGC 649
Db 777 GGAGATATTTTTCACAAATTCATTTGTTGGAGTTTGGAGAAATCTGATCGTCTCTGCTGCTGC 836
Qy 650 AATAGCCCAAGAACAGAAATCTGCATCACCCTGATCTTTTTCATCTCTAGCTGCTGCTGCT 709
Db 837 TGTGTTCAAGAAATAGAAATCTCCAGGACCCCTGATCTTTTTCATCTCTAGCTGCTGCTGCT 896
Qy 710 GCGGATATGCTGGTGGAGCTTTTCAACGGGTTCAGAGACCATCGTCAATCACCCTGTTGAA 769
Db 897 ATCTGATATGCTGGCAGCCTATATAGATCTTGGAAATATCTGATCATATTCAGAGAA 956
Qy 770 CA---GTACGATACGGACGCGAGTTTCAOOGTGAATATTTGATAATGTCATGACTC 826
Db 957 CATGGCATACTCAAGCCACGCTGGCAGTTTGAACACACAGCCCATGACATCATGACTC 1016
Qy 827 GGTATCTGTAGCTCTCTGCTGCGCTGATGAGCCCTGCTCTCAATTCAGTGCAGTGCAG 886
Db 1017 CTTGTTCTGCTCTCCGCTCTTGGCTCCATCTTCGACCTGCTGCTGCTGCTGCTGCTGCTG 1076
Qy 887 GTACTTTACTATCTTTTATGCTCCCTCCAGTACCATCAATCAATGACGGGTGAGCGGGTTGG 946
Db 1077 CTACATCAATCTTCCAGCAGCTGCGGTACACAGCATGCTGACCATGCGCGGCACATGT 1136
Qy 947 GATCATCATCAGTTGCAATCTGGGCGCTTGCACGGTGTGACGGTGTGACGACATCTTTTTCATCATTTA 1006
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Qy 1007 CTCGACAGTACTGCTGTCATCATCTGCTCATCACCCTGCTCTTCCACCATGCTGCGCTT 1066
Db 1197 CTCCCATCATGTGCCACGCTGACCTTCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTT 1256
Qy 1067 CATGGTCTCTCTACGTCACCATGTTCTCTCATGGCCAGCTGACATCAAGAGAAATCGC 1126
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Qy 1127 CGTCTCCGGGACACGGCACCATCCGCAAGGGGCCAACATGAAGGTGCTGCTGCTGCTGCTG 1186
Db 1317 CACCTCCCCAGA-----GCCAACAATGAAGGGGCCATCACACT 1355
Qy 1187 GACCATACCTATTGGGGTCTTCGGTCTGGCTCCCATCTTCTCCACTTGATATT 1246
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Qy 1247 CTACATCTCTGTCCCGAAGATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1306
Db 1416 GATGACATCTGCTCCCAAGTAACTCCCTACTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1475
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RESULT 15

US-10-015-948-1
; Sequence 1, Application US/10015948
; Patent No. US20020133843A1
; GENERAL INFORMATION:

